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15467

From:

Whiteman, Brian

Sent:

Friday, May 27, 2005 9:45 AM STIC-Biotech/ChemLib

To:

Subject:

seq search

09/610,313 Barnett et al.

SEQ ID NOs: 30, 31, and 32

- nucleotide search against databases
 amino acid search against databases

Thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

> Type of Search Interference:___ _Oligomer:_ S/L:____ Encode/Transl:

> > Text:

Structure#:_

Inventor:____ Litigation:_

Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT:_ LEXIS/NEXIS:_ SEQUENCE SYSTEM: WWW/Internet:_ Other(Specify):_

STAFF USE ONLY Searcher: Searcher Phone: 2-Date Searcher Picked up:_

Online Time:_

Date Completed: 4/3
Searcher Prep/Rev. Time:

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Compugen Ltd.
GenCore version
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nucleic search, using sw model OM nucleic

Run on:

May 31, 2005, 23:20:00 ; Search time 1270.42 Seconds (without alignments) 11504.726 Million cell updates/sec

US-09-610-313B-30 2469 score: Title: Perfect

1 gtcgacgccaccatggccga......gggctagcaccggtgaattc 2469 Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 seg seg 88 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* •• Database

geneseqn1990s:* geneseqn200s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* genesegn2003cs:* genesegn2003ds:* geneseqn2003as:*geneseqn2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

	Description	Abl39959 Synthetic	Adm73764 HIV-1 pol	Aca03548 Synthetic	Adc13266 DNA of HI	Abl39960 Synthetic	Adm73765 HIV-1 pol	Aca03547 Synthetic	Adc13265 DNA of HI	Abl39961 Synthetic	Adm73766 HIV-1 pol	Aca03546 Synthetic	Adc13264 DNA of HI	Adc13230 DNA of HI	Adc13231 DNA of HI	Adc13232 DNA of HI	Aca03591 Synthetic	Adc13279 DNA of HI	Adc13234 DNA of HI	Adc13236 DNA of HI	Aca03521 Synthetic	
SUMMARIES	QI.	ABL39959	ADM73764	ACA03548	ADC13266	ABL39960	ADM73765	ACA03547	ADC13265	ABL39961	ADM73766	ACA03546	ADC13264	ADC13230	ADC13231	ADC13232	ACA03591	ADC13279	ADC13234	ADC13236	ACA03521	
	DB	9	12	ω	10	9	12	ω	10	9	12	60	10	10	10	10	ω	10	10	10	80	
	* Query Match Length DB	2469	2469	2457	2457	2463	2463	2457	2457	2457	2457	2445	2445	3930	3930	3930	5184	5184	3531	3537	5145	
	% Query Match	100.0	100.0	99.5	99.5	98.9	98.9	98.6	98.6	97.8	97.8	97.3	97.3	97.0	6.96	6.96	6.96	96.9	95.7	92.6	92.6	
	Score	2469	2469	2457	2457	2442.2	2442.2	2434.6	2434.6	2415.4	2415.4	2401.8	2401.8	2394.8	2393.2	2393.2	2393.2	2393.2	2362.8	2361.2	2360.2	
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Adc13233 DNA of HI	Synth	Adc13268 DNA of HI	S	Adc13269 DNA of HI	Aca03549 Synthetic	Adc13267 DNA of HI	Aca03543 Synthetic	Acc78507 HIV p2Pol	Aca03542 Synthetic	Acc78506 HIV p2Pol	Aca03541 Synthetic	Acc78505 HIV p2Pol	Acc78488 HIV GagPo	Acc78489 HIV GagPo	Aca03522 Synthetic	Adc13238 DNA of HJ	Acc78484 HIV GagCo	Acc78485 HIV GagCo	Acc78486 HIV GagCo	Aca03584 Synthetic	Acc78529 HIV TatRe	Aca03592 Synthetic	Adc13280 DNA of HI
ADC13233	ACA03550	ADC13268	ACA03551	ADC13269	ACA03549	ADC13267	ACA03543	ACC78507	ACA03542	ACC78506	ACA03541	ACC78505	ACC78488	ACC78489	ACA03522	ADC13238	ACC78484	ACC78485	ACC78486	ACA03584	ACC78529	ACA03592	ADC13280
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95.6	95.2	95.2	93.2	93.2	92.5	92.5	87.1	87.1	85.9	85.9	84.8	84.8	84.8	84.8	84.8	84.8	84.6	84.5	84.5	84.5	84.5	84.5	84.5
2360.2	2349.4	2349.4	2301.8	2301.8	2283.6	2283.6	2149.6	2149.6	2121.2	2121.2	2094.4	2094.4	2093.4	2093.4	2092.8	2092.8	2089	2087.4	2087.4	2087.4	2087.4	2087.2	2087.2
21	23 23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds. Synthetic construct PR975(+) SEQ ID NO:30 Human immunodeficiency virus; type C. BP. 05-JUL-2001; 2001WO-US021241. ABL39959 standard; DNA; 2469 05-JUL-2000; 2000US-00610313. (first entry) (CHIR) CHIRON CORP. (UYST-) UNIV STELLENBOSCH. WO200204493-A2. 17-JAN-2002. 15-MAY-2002 Synthetic ABL39959; RESULT 1 ABL39959

Zur Megede J, Barnett SW,

Van Rensburg Engelbrecht S, WPI; 2002-154920/20.

Ε,

New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.

Claim 1; Fig 8; 233pp; English.

The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gay, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (1). (1) have immunostimulant activity and can be used in gene therapy.

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The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV
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& <u>a</u>	901	TTCCGCGAGCTGAACAAGGGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 960
È	961	CGGCCTGAAGAAGAAGAAGGGGGGGGGGGGGGGGGGGGG
Db	961	CCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCTGCTGGCTG
કે દ	1021	AGGGGGCCCTGGACGACGACTTCCGCAAGTACACGCCTTCACCATCCCCAGCATCAAC 1080
i è	1081	AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC 1140
QQ	1081	AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC 1140
<u>ک</u> ج	1141	CCCAGCATCTTCCAGAGCAGGATGACCAGATCCTGGAGCCCTTCCGCGCCCGCACCCC 1200
l &	1201	GAGATCTGCGACTTACCAGTACATGGACGACCTGTACGTGGGCGCGCACCTGGAGATCGGC 1260
qq	1201	GAGATCGTGATCTACCAGTACATGGACGTCTGTACGTGGGCAGCGACCTGGAGATCGGC 1260
ò	1261	CAGCACCGCGCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTCGGGCTTCACCACC 1320
Ωp	1261	CAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGGCTTCACCACC 1320
<u>ک</u> ج	1321	CCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGTGCACCCC 1380
ìò	1381	GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGCTGGACCGTGAACGAC 1440
Db	1381	
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Dp	1561	GAGGAGGCCGAGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCGTGCAGCC
È		SACCAG 1
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8 8	1681	TACGCCAAG 1
a S	68	CCTACCAGATCTACCAGGGGCCCTTCAGGAACCGGAAGACCGGCAAGATACGCAAG 1
÷ €	1741	, 0
3 8	. 0	186
음 전	1801	ATGGAGACATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCAGAAGGAG 1860
λΌ	1861	rggagrrc 192
Db	1861	GGAGTTC 192
δ		ATCGGC 1
Dp	1921	aaacacccccccagaagctgtacgaacctggagaaggagaagagcccatcatcggc 198
δλ	1981	GCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGC 2040

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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
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100.0%; Pred. No. 7.4e-298;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                               Sequence 2469 BP; 571 A; 833 C; 761 G; 304 T; 0 U; 0 Other;
      Claim 1; SEQ ID NO 30; 160pp; English.
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Matches 2469; Conservative
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                                                                                                                                                                                                                                     ACCGAGCTGCAGGCCATCCAGCTGGCCTGCAGGACAGCGGCAGGAGGTGAACATCGTG
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human immunodeficiency virus immunogenic peptide
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126 GCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCAC 180 246 240 306 300 366 360 426 420 486 480 546 540 909 9 AACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGGAAGGAGGGCCACATC 120 GGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCTGCACCCTG 666 99 9 CAGATGAAGGACTGCACCGAGCGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCC CAGGGCAAGGCCCGCGAGTTCCCCAGCGAGAAACCGCGCCAACAACAGCCCCAACAGCCGC GAGCTGCAGGTGCGCGCGCGCAACCCCCGCAGCGAGCCCGGCGCCCGAGCGCCCAGGGCACC CTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGC CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTTCGGCGGCGCTTCATCAAGGTGCGC CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGC GCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCCCAACATCCTGATGCAGCGCAGC AACTTCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATC GCCCGCAACTGCCGCGCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGGCCCAC CAGATGAAGGACTGCACCGAGCGCCAAGCTTCTTCCGCGAGGACCTGGCCTTCCCC CAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCAACAGCCGC GAGCTGCAGGTGCGCGGCGACAACCCCCGCAGGGGGGGCGGCGGCGGCGCCAGGGCAACC CAGATCAAGGAGGCCCTGCTGGACACCGGCGGACGACGACGACGTGCTGGAGGAGGATGAGC CAGTACGACCAGATCCTGAGATCTGCGGCAAGAAGGCCCATCGGCACCGTGCTGATC CAGTACGACCAGATCCTGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATC GCCACCATGGCCGAGGCCATGAGCCAGGCCCACCAGCGCCCAACATGCTGATGCAGCGCAGC CAGATCAAGGAGGCCCTGCTGGACACCGGCGGCGACGACGACGTGGAGGAGATGAGC Gaps ö Length 2457; 0; Indels 99.5%; Score 2457; DB 8; L. llarity 100.0%; Pred. No. 2.3e-296; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 2457; Conserv 247 Н 67 61 121 541 607 127 187 181 241 307 301 367 361 427 421 487 481 547 g Š 셤 g 8 8 g 셤 셤 g ઠ ઠે g 6 6 6 8 ઠે ઠે

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type C; gene therapy; vaccine; immunisation; HIV; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel expression cassette comprising a polymucleotide sequence encoding a polymptide including an HIV Gag, Int., Nef, pl5RnaseH, Pol, Tat, Prot, or Rev polymptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramocally, intravasion, intraversion, production of the expression cassette is use for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymuclectide sequence represents the DNA of an Hive Type C related sequence of the invention.
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                                                                                                                                           멼.
                                                                                                                                              Van Rensburg
                                                                                                                                                                                                                            New expression cassette comprising a polynucleotide sequence encopolypeptide including an HIV Gag, Env. Int. Nef. plSknaseH, Pol., Prot., or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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100.0%; Pred. No. 2...
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                           SW,
                                                                       CHIRON CORP.
UNIV STELLENBOSCH
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Best Local Similarity 100.
Matches 2457; Conservative
                                                                                                                                              Barnett
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1681 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGGCAAGTACGCCAAGATGCGC 1740 2100 2166 2220 2346 2340 2406 2463 nef; 2457 ACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAAGAAGAACGAG CACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG ACCGCCCACACCAACGACGTGAAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG GAGACCTGGTGGACCGACTACTGGCAGCCCACCTGGATCCCCCGAGTGGGAGTTCGTGAAC GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGGAGTTCGTGAAC 1927 ACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG ACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG ACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAAGGCCGGCTACGTG AGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCGAGGCGAGTG CACAAGGGCATCGGCGCGCCAACGAGCAGATCGACAAGGCTGGTGAGCAAGGGCATCCGCAAG AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; immunostimulant; gene therapy; gene; ds. TACGTGGGCGGCGGCCCTAGGATCGATTAAAAGCTTCCCCGGGGCTAGCACCGGT TACGTGGGCGGCGGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGGCTAGCACCGGT

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GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG
                    ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG
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                                                                                                                                                                                                                                                                                                            The present invention describes expression cassettes comprising a polynuclectide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gay, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABBBG204 to ABBBG215 represent sequences used in the exemplification of
                                                                                                                                                                                                           New polynucleotides encoding antigenic HIV Type C polypeptides, useful i applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.
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                                                                                                                                                   Engelbrecht
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                                   05-JUL-2001; 2001WO-US021241
                                                                   2000US-00610313
                                                                                                                                                   SW.
                                                                                                                   UNIV STELLENBOSCH
                                                                                                                                                   Zur Megede J, Barnett
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Human immunodeficiency virus 1.
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Matches 2460; Conservative
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BARNETT S W.
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HIV type C protein; immunostimulant.
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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements comparible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                             New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCACCAGATGAAGGACTGCACCGAGCGCCAAGCTTCTTCGGGAGGACCTGGCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2463 BP; 567 A; 835 C; 759 G; 302 T; 0 U; 0 Other;
EJV;
         Rensburg
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Engelbrecht
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                        AGCCGCGAGCTGCAGGTGCGCGGCGAAACCCCCGCAGCGAGGCCGGCGGCGGCGAGCGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a synthetic polymucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polymucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polymucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polymucleotide is also useful for DNA immunisation of, or for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TTCCCCCAGGCAAGGCCCGCGAGTTCCCCAGCGAGAACCGCGCCAACACGCCCCACC 300
                                                                                                                                     Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic polynucleotides encoding antigenic HIV type B and/or type (polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
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                                                                                             Synthetic DNA ecoding immunogenic HIV peptide #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2434.6; DB 8 Pred. No. 1.4e-293;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349793P.
16-JAN-2002; 2002US-0349871P.
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Matches 2453; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          expression cassette; HIV Gag; Env; Int; Nef; p15RnaseH; Pol; Tat; Prot; Rev; HIV type C; gene therapy; vaccine; immunisation; HIV; ds.
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Pred. No. 1.4e-293;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                             ADC13265 standard; DNA; 2457
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                                CGCAAGGTGCTGTTCCTGGACGCATCGATGGCGGCATCCTGATCTACCAGTACATGGAC
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iive 0; Mismatches 6;
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Matches 2451; Conservative
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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements comparible polynucleotide sequence further comprises control elements comparible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
       CTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTG
                                                           CCGCCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAAGCAAGGGCATC
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HIV type C protein; immunostimulant.
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(BARN/) BARNETT S W.
(ENGE/) ENGELBRECHT
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Query Match 97.8%; Score 2415.4; DB 12; Length 2457; Best Local Similarity 99.3%; Pred. No. 3.3e-291; Matches 2451; Conservative 0; Mismatches 6; Indels 12; Gaps 2; Qy GTGGAGGCCATGAGGCCATGAGCCACAGGGCCAACATCCTGATGCAG 60 Db GTCGACCACATGAGGCCATGAGCCACAGGGCCACAGGGCCAACACATGCAG 60 Qy GTCGAGCACTTCAAGGGCCCCAAGGGGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120 Qy GGCAGCAACTTCAAGGGCCCCAAGGGGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120 Db GGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120	Oy 121 CACATGGCCGGCAACTGCCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG 180 Db 121 CACATCGCCCGCAACTGCCGCCCCCCGCAAGAAGGGCTGCTGGAAAGTGCGGCAAGGAG 180 Qy 181 GGCCACCAGATGAAGGACTGCACGAGCCCAACTTCTTCCGCGAGGACTGGCC 240 Db 181 GGCCACCAGATGAAGGATTGCACGAGGCCCAAGTTCTTCCGCGAGGACTTGGCC 240	241 TTCCCCCAGGGCAAGGCCCGGAGTTCCCCAGGGAGCAGAACGGCCCAACAGCCCCACC 30 [3GTG 42 3GTG 42 3GTG 42		541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG 60 541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG 60 541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG 60 601 CTGATCGGCCCCACCCCGTGAACATCGGCCGAACATGCTGACCTGACCCAGCTGGGCTGC 66	601 CTCGAACTTCCCCATCCACCCCATCCACCACACAACATGCTCACCTGAGCTGC 661 ACCTGAACTTCCCCATCCACCATCATCATCAGCCTGCACATGAACTTGAAGCTGGGCTGT 7 661 ACCTGAACTTCCCCATCGAGCCCATCGAGCTGCCGTGCAAGCTGAAGCTGGAACTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCCCCATTCCAAGCCCCATTGCAAGCCCGATGCCCGATGCCGAAGCTGAAGCTGAAGCTCGAAGCCCCATTCCAAACTGAAGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGATGCCCGAAGCTGAAGCCCGATGCCCAATG	721 GACGCCCCAAGGTGAAGCAGTGGCCCCTGACCAAGAGAAGATCAAGGCCCTGACCGCC 78		901 TTCCGCGAGCTGAACAAGCGCACCCAAGAACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC

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polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
                                                                                                                                                                                                                                                                                                                                               AACTTCAAGGGCCCCCAAGCGCATCATCAAGGGCTTCAACTGCGGCAAGGAGGGCCACATC
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                                                                                                                                                       Sequence 2445 BP; 562 A; 835 C; 751 G; 297 T; 0 U; 0 Other;
                                                                                                                                                                                     Score 2401.8; DB 8
Pred. No. 1.6e-289;
0; Mismatches 7;
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0
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Best Local Similarity 99.2
Matches 2438; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV
                     ACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTG
                                                    ACCGACAGCAGTACGCCCTGGGCATCATCCAGGCCCCAGCCGACAAGAGCGAGAGCGAG
                                                                          ACCGACAGCCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGGGAG
                                                                                                                      CTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTG
                                                                                                                                                      creergaaccagarcarcagcagcrearcaagaagaagaagarcreagcreegre
                                                                                                                                                                                                                                                          CGCAAGGTGCTGCTGCTGGACGCCATCGATGGCGCCATCGTGATCTACCAGTACATGGAC
                                                                                                                                                                                         CCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; va
gene therapy; packaging cell line; humoral immune response;
cellular immune response; gene delivery vector; DNA immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide #29.
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349728P.
16-JAN-2002; 2002US-034973P.
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Rev; HIV type C; gene therapy; vaccine; immunisation; HIV; ds
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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16-JAN-2002; 2002US-0349871P.
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                                                                                                   The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV dag, Int., Nef. p15RnaseH, Pol., Tat., Prot., or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intransally, intranscularly, intransdermally, intranscularly, intravenously, intra
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polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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Rev, HIV type C, gene therapy, vaccine; immunisation; HIV; ds
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31-AUG-2001; 2001US-0316860P.
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                                                                                                                                                                                                                  The invention relates to a novel expression cassette comprising a polymorleotide sequence encoding a polympetide including an HIV Gag, Enr, Nef, piSmasseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intravectally, orally or intravenously. The expression cassette is useful point immunisation, generating packaging cell lines and producing HIV polypeptides. This polymucleotide sequence represents the DNA of an HIV Type C related sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCA 1726
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New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3930;
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Pred. No. 1.7e-288;
0; Mismatches 8; Indels
                                                                                                                                                                  Disclosure; Fig 8; 301pp; English.
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Matches 2430; Conservative
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Oy 1814 TGATCTGGGGCAAGACCCCC Db 3275 TGATCTGGGGCAAGACCCCC Oy 1874 GGTGGACCGACTACTGGCAG Oy 1875 GGTGGACCGACTACTGGCAG Oy 1936 CCCTGGTGAAGCTGTGGTAG Db 3395 CCCTGGTGAAGCTGTGGTAC	Oy 1994 ACCTGGACGCGCCGCAAC Db 3455 ACCTGGACGCGCGCCAAC OY 2054 GGGGCGGCAGAAGATCGTC Db 3515 GGGCCGGCAGAAGATCGTC OY 2114 CCATCCAGCTGGCCTGCAC Db 3575 CCATCCAGCTGGCCTGCAGAACATCGTC Db 3575 CCATCCAGCTGGCCCTGCAG	0y 2174 ACGCCTGGGCATCATCCAC 0b 3635 ACGCCTGGGCATCATCCAC 0y 2234 TCATCGGGCACTGATCAAC 0y 2294 GCATCGGCGGCACTGATCAAC 0y 2294 GCATCGGCGCAACGAGCAC 0y 2294 GCATCGGCGGCAACGAGCAC 0y 2354 TCCTGGACGCGCAACGAGCAC 0y 2354 TCCTGGACGCGCAACGAGCAC 0y 2354 TCCTGGACGCGCAACGAGCAC 0y 2414 GCAGCGGCGCCATCGATCGATCGATCGATCGATCGATCGA	Search completed: June 1, 2005, Job time: 1280.42 secs
2147 CCATCAGCCCCATCAAACCTGCAAACCTGAAGCCCGGCATGGACGCCCCAAGG 2206 734 TGAAGCAGTGGCCCCTGACGAGAGAACATCAAGCCCTGACGCCCCCAAGG 2206 734 TGAAGCAGTGGCCCCTGACCGAGGAGAACATCAAGGCCCTGACCGCCATCTGCGAGGAGA 793 2207 TGAAGCAGTGGCCCCTGACCGAGGAGAACATCAAGGCCCTGACCGCCATCTGCGAGGAGA 2266 794 TGGAGAAGAGAGAAGATCACAAAATCACCCCTGACAACACCCCCGTG 853 2267 TGGAGAAGGAAGATCACCAAGATCGGCCCCGAAAACCCCTACAACACCCCCGTG 2326 854 TCGCCATCAAGAAGAACAACAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGT 2326 855 TCGCCATCAAGAAGAACAACAAGAACGGCCCAAGAACTGCCCCAACAACTCCGCGAAGATCGGCCCAAGAACCCCCCTACAAACACCCCCCTTATTTTTTTT	2327 TCGCCATCAGAAGAAGAACGACCAAGTGGCGCAAGTGGCACAGTGGAACTTCCGCGAGCTGA 2386 914 ACAAGCCACCAGGACTTCTGGGAGGTGCAGCTGGCATCCCCCCCC		TGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACGATCCAGAAGCTGG 14 TGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGATCCAGAAGCTGG 29 TGGGCAAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGATCCAGAAGCTGG 29 TGGGCAAGCTGAACTGGGCCAGCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCA 15 TGGGCAAGCTGAACTGGGCCAGCAGTTCTACCCCGGCATCAAGGTGCGCCAGCTGTGCA 29 AGCTGCTGCGCGCGCCAAGGCCCTGACCGAATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCA 30 TGGAGCTGGCCGAGAACCGCAAGACCCGAACCCGAGCCTGACCGAGCGAG

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GCGCCATCGTGATCTACCAGTACATGGACGACCTGTACGTGG 2413 1993 TGAGCCTGACCGGACCACCAACCAAGAGGCCGAGCTGCAGG 2113 AGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGT 2173 AGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCAAGG 2293 CCAAGTICCGCCTGCCCATCCAGAAGAGACTGGGAGACCT 1873 AGCCACCTGGATCCCCGAGTGGGGTTCGTGAACACCCCCC 1933 ACCECCAAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACC 2053 ACCAGCTGGAGAAGGAGCCCATCATCGGCGCCCGAGACCTTCT

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AF287355 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zur Megede,J., Barnett,S.W., Engelbrecht,S. and van Rensburg,E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof Patent: WO 0204493-A 30 17-JAN-2002; CHIRON CORPORATION (US); University of Stellenbosch (ZA) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCCAACATCCTGATGCAG
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|mol_type="unassigned DNA"
|Ab_xref="taxon:32630"
|note="PR975(+)"
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synthetic construct
other sequences; artificial sequences.
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AX427926 Sequence
AX427927 Sequence
AX427936 Sequence
AX427938 Sequence
AX427938 Sequence
AX427938 Sequence
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AX455915 Sequence
AX455916 Sequence
BD263706 Improved
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Compugen Ltd.
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                 GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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ı	f AN-2002; iversity of Stel	a &	841 AACACCCCCGTGTTCGCCATCAAGAAGAAGAACAGCACCAAGTGGCGCAAGCTGGTGGTGGTCCCCCCCC
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TGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG
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TGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGG
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                                                                Gaps
                                                               12;
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                                             Score 2052; DB 6;
Pred. No. 9.6e-206;
0; Mismatches 135;
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                                             Match 83.1%;
Local Similarity 93.6%;
es 2165; Conservative
                                                       Best Local Sim:
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Expression of HIV polypeptides and production of virus-like
                                                                                                                                                Length 2312;
                                                                                                                                                                                 Indels
                                                                                                                                              Score 2052; DB 6;
Pred. No. 9.6e-206;
0; Mismatches 135;
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Patent: US 6602705-A 84 05-AUG-2003;
Location/Qualifiers
                                                                                                  DNA.
                                                                               /organism="unknown"
/mol_type="genomic |
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Best Local Similarity 93.6%;
Matches 2165; Conservative
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Barnett,S.W., Megede,J., Greer,C. and Selby,M.
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	X427930 Squence 168 from Patent W00232943. X427930. X427930.1 GI:21538017 Ynthetic construct Ynthetic construct Ynthetic construct ther sequences; artificial sequences. Uang,Y. and Nabel,G.J. Odifications of hiv env, gag, and pol enhanentic immunization atent: WO 0232943-A 168 25-APR-2002; OVERNMENT OF THE UNITED STATES (US) Location/Qualifiers 1. 9166 Organism="synthetic construct" //mol_type="unassigned DNA" //db_xref="taxon:32630" //noTe="plasmid pVR1012x/s containin" //noTe="plasmid pVR1012x/s containin"	Dest Local Similarity 92.64; Pred. No. 8.2e-206; Matches 2192; Conservative 0; Mismatches 163; Indels 13; Gaps 3; Matches 2192; Conservative 0; Mismatches 163; Indels 13; Gaps 3; QY 14 TGGCCGAGGCCATGAGCACGCCCACCGCGCAACATCCTGATGCAGCGCACACTCA 73
1058 CCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCTACCAGTACAACGTGC 1117 901 CCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCTACCAGTACAACGTGC 960 1118 TGCCCCAGGGCTGGAAGGGCACCCCCGGCTACCAGTACCAGTACCAGTGCCAGTTACCAGTGCCAGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCAGGCTGCCCAGGCTGCCCAGGCTGCCCAGGCTGCCAGGCTGCCAGGCTGCCCTGCGGCTGCCCTGCGCTGCCCTGCGCTGCCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	AGGAGACTGGACCGTGAACGACATCCAGAAGCTGGGCCAGCCGCCGCCGCCGCCGCGCGCG	173 CCGAGGCCGAGGAGGCATCGTGATCGTGATCGTGATCGTGATCGTGGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCCCCAAGT 1837 1621 CCGAGGCCGTGCAGGAGCCCCCAAGT 1680 1838 TCCGCCTGCCCAGTCGAAGGCCCCAGGCCAGGTGGAGCCCCAGGTGGAGCCCCAGGTGGAGCCCCAGGTGATCGCGAGGCCAGGTGATCGTGAACCCCCCTGGTGGATCGTGAGGCAGCCCAGGTGAGGCCCATCCAGGAGGCCCCTGGTGGATCGTGAACCCCCCCTGGTGAACGCGCCCCAGGTACTGGCAGGCCCAGGTGAGGCCCAGGAGCCCCCCCTGGTGAACGCCCCCAACCGCC 1957 1741 CCTGGATCCCCGAGTCGAGGAGCCCCAGCCCCCCTGGTGAAGGTCGCCAACCGCC 2017 1741 CCTGGATCCCCAGGAGGCCCCAGCCCCCCTGGTGAAGGTCGCCCAACCGCC 2017 1801 TGGAGAAGGAGCCCATCGTGACCCCCCCCCTGGTGAACGCCCCCAACCGCC 2017 1801 TGGAGAAGGACCCCATCGTGACCCCCCCCCCCCCCCAGGCCCCCAACCGCC 2017 1801 TGGAGAAGGCCCCAACCGCCCCCCCCCCCCCCCCCCCCC

1412 TCCNANGCCGROCAGCCCATCGTGCTGCCCGAAACTTACCCGGGCTCAAGGTCC 1501 1412 TCCNANGCTGGTGCTGAACTTGGCCCGCGCACTTACGGCCGGCATCAAGGTCC 1501 1410 TCCNANGCTGGTGGCTGAACTTGGCCCGGCACTTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCGCACATCTACGGCGCACATCTACGCGCGCACATCTACGCGCGCACATCTACGCGCGCACATCTACGCGCGCACATCTACCGCGCACATCTACCGCGCGCACATCTACCGCGCGCACATCTACCGCGCACATCTACCGCGCACATCTACCCCCTACACATCTACCACATCTACCACATCTACCACATCTACCACACATCTACCACACATCTACCACACATCTACCACACACATCTACCACACACACACACACACACACACACACACACACACACA	Db 5300 GCAAGGTGCTGTTCCTGGACGGCATCGA 5327 RESULT 8 AX427936 LOCUS AX427936 DEFINITION Sequence 174 from Patent W00232943. ACCESSION AX427936 VERSION AX427936.1 GI:21538023
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Pred. No. 6.1e-205;
0; Mismatches 177; Indels
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1. 9788
7. organism="synthetic construct" |
/mol_type="unassigned DNA" |
/db_xref="taxon:32630" |
/note="plasmid pVR1012x/s containing
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                                             Huang, Y. and Nabel, G.J.
Modifications of hiv env, gag, and pogenetic immunization
Patent: WO 0222943-A 174 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
synthetic construct
synthetic construct
other sequences; artificial
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Best Local Similarity 91.8%;
Matches 2197; Conservative 0
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               CCTGGGAGGCCTGGTGGACCGAGTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCG
                                                                  TGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGGAGCCCATCATCGGCG
                                                                                                                         ACGTGACCGACCGCGGCCGCAGAAGGTGGTGCCCTGACCGACACCACCACCAGAAGA
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                                                       TGAACACCCCCCCCCCGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG
                                                                                                           CCGAGACCTTCTACGTGGACGCCGCCGAACCGCGAGACCAAGATCGGCAAGGCCGGCT
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Modifications of hiv env, gag, and pol enhance immunogenicity genetic immunization
genetic immunization
Patent: WO 022943-A 169 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
1. 9169
/ organism="synthetic construct"
//mol_type="unassigned DNA"
//db xtref="taxon:32630"
//noTe="plasmid pVR1012x/s containing HIV genes"
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Pred. No. 1.8e-203;
0; Mismatches 182; Indels
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Sequence 169 from Patent W00232943.
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Best Local Similarity 91.7%;
Matches 2194; Conservative
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VERSION
KEYWORDS
SOURCE
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AX427931
LOCUS
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Db 5243 CCGCCCACAAGGGCATCGGCGAACGAGCAGGTGGACGGCCTGGTGAGCGCCGGCATCC 5302 Qy 2342 GCAAGGTGCTGTTCCTGGACGCATCGATGGCGGCATCTACCAGTA 2393	RESULT 10 AX427925 LOCUS AX427925 LOCUS BEFINITION Sequence 163 from Patent W00232943. ACCESSION AX427925 VERSION AX427925 VERSION AX427925.1 GI:21538012	W ш	AUTHORS Huang, Y. and Nabel, G.J. TITLE Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization JOURNAL Petent: WO 023943-A 163 25-APR-2002;		/mol_tref="taxon:3580" /db_xref="taxon:3580" /note="plasmid pVR10i2x/s containing HIV genes" ORIGIN	Query Match 82.1%; Score 2027; DB 6; Length 9194; Best Local Similarity 91.6%; Pred. No. 2.8e-203; Matches 2194; Conservative 0; Mismatches 185; Indels 16; Gaps 4;	Oy 14 TGGCCGAGGCCATGAGCCAGGCCACCAGGCCAACATGCTGATGCAGCGCAGGAACT 70	Oy 71 TCAAGGCCCCAAGCGCATCATCAACTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCC 130	Qy 131 GCAACTGCCGCCCCCGCAAGAAGGCTTGCTGGAAGTGCGGCAAGGAGGCCCACCAGA 190 100 100 101 100 102 3087 103 3087 104 3087 105 3087 106 3087 107 3087 108 3087 109 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087 100 3087	OY 191 TGAAGGACTGCACGCCAGGCCAACTTCTCCGCAAGGACCTGCCCTTCCCCCAGG 250	OY 251 GCAAGGCCCGCAAGTTCCCCAGCAGAACCGCGCCAACAGCCCCACCAGCGGGGGGG	Oy 311 TGCAGGTGCGGGCGACAACCCCGCAGGGGGGGCGGGCCGAGGCCCAGGGCA 364	Oy 365CCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAGG 418 Db 3326 CTGTATCCTTTAGCTTCCCTCAGATCACTCTTTGGCAGCGACCCCTGGTCACAATAAAGA 3385	OY 419 TGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGCCGTGCTGGAGG 478	QY 479 AGATGAGCCTGCCCGGCAAGTGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA 538 Db 3446 AGATGAACCTGCCCGGCCGCTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCA 3505	Qy 539 AGGTGCGCCAGTACGACCAGATCCTGATCTGCGGCAAGAAGCCATCGGCACG 598
	1322 CCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGACCTGCACCCCG 1381		1502 GCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG 1561 	1562 AGGAGGCCGAGCTGGAGCCGAGAACCGCGAGATCCTGCGGGGGCCCGTGCACGGCG 1621 	1622 TGTACTACCACCCCAGCAAGCACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAGT 1681	1682 GGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCGAGTACGCCAAGA 1741 	1742 TGCGCACCCCCACACCACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA 1801 	1802 TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1861 	1862 CCTGGGAGACCTGGTGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGACTTCG 1921 	1922 TGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG 1981	1982 CCGAGACCTTCTACGTGGACGGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGGT 2041	2042 ACGTGACCGACGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAACCA	2102 CCGAGCTGCAGCCATCCAGCTGGCCCTGCAGGACAGCGGAGGTGAACATGTGA 2161	2162 CCGACAGCCAGTACGCCTGGGCATCATCCAGGCCCAGCCGGACAGAGCGAGAGCGGGC 2221	2222 TGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGC 2281	2282 CCGCCCACAAGGGCATCGGCGGCAACGAGCAAGCTGGTGAGCAAGGCAAGGGCATCC 2341

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619 AGTGGACCTACCAGATCTACCAGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCA 4646 AGTGGACCTACCAGATCTACCAGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCC 1739 AGATGCGACCCCACCACCACGACGTGAAGACCGGAGCCGGCGCAGAAGATCG 1739 AGATGCGCACCCCCACCACGACGTGAAGACCGCTGCCGAGGCCGTGCAGAAGATCG 1739 CCATGGAGGCATCGTGATCTGGGGCACACGAGCCGTGCCAGAGAGTCG 1730 CCATGGAGGCATCGTGATCTGGGGCACACGAGCCGTGCAGAGATCG 1730 AGATCTGGAGACCTGATCGTGACCCTCCAAGAGTCGCCAAGAGTCG 1730 AGATCTGGAGACCTGATCGTGACCCCCCAAGAGTCCAAGAGTCG 1730 AGATCTGGAGACCTGATCGTGACCCCCCCAAGAGTCCCCAAGAGTCGCCAAGAGTCG 1730 AGACCTGGAGACCTGATGATCTGGGAGCCCCCCCCAAGATCCAAGAGTCG 1850 AGACCTGGAGACCCTGATGATCTGGCAGCCCCCCCCAAGAGTCCCCAAGAGTCCCCAAGAGTCCCCCAAGAGTCCCCAAGAGTCCCCCAAGAGTCCCCCAAGAGTCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCAAGAGTCCCCCCCC	Db 5246 TGCCGCCCACAAGGCCATCGGCGCCAACGAGCAGCGCCGGCA 5305 Qy 2339 TCCGCAAGGTCTGTTCCTGGACGCATCGTGATCTGCAGTA 2393
3506 AGGTGGGCCACTACGATCCTGATCGACCACACTGGGCCACAGGCCACCGGGCCCGGGCGGG	

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1019 TCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 10 3986 TCAGCGTGCCCCTGGACAAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCA 10 1079 ACAACGACACCCCGGCATCCGCTACCAGTACAACGTCTGCCCAGCGCTCCAGCATCA 40 1079 ACAACGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCA 11 4046 ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCA 41 1139 GCCCCAGCATCTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACC 11 1130 GCCCCAGCATCTTCCAGAGCACAAGATCCTGGAGAGCCCTTCCGCGCCCGCAACC 11 1110 GCCCCCAGCATCTTCCAGAGCACAAGATCCTGGAGGCCCTTCCGCGCCCGCAACC 11 1106 GCCCCGCCATCTTCCAGTGCAACCAAGATCCTGGAAGCCCTTCCGCAAGAACC 41	Oy 1199 CCGAGATCGTGACTGTACCAGTACATGACGACCTGTAGGAGGACCTGGAGATCG 1259 CCGAGATCGTGACCAGTACATGAGACCTGTACATGGACCTGGAGATCGGAGCTGGAGATCGGAGCTGGAGATCGGAGCTGGAGATCGGAGCTGGAGATCGGAGCTGCAGACCTGCTGGAGATCGAGGACCGCAAGATCGAAGATCGAGAGCTGCAAGATCGAAGATCGAAGATCGCAAGATCGCAAGATCGAGGACTGCCCAGCACCTGCGGCTTCACCA 131 Oy 1259 GCCAGCACCGCAAGATCGAGAGCTGCCAAGCACCTGCTGCTGCGCTTCACCA 131 Ob 4226 GCCAGCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGCGCTGGGGCTTCACCA 428	Oy 1319 CCCCGACAAGAACACCACAGAAGGACCCCCCTTCCTGGATGGGCTACGAGCTGCACC 137	1439 ACATCCAGAAGCTGGGGCAACTGGGCCAGCCAGATCTACCCGGCATCAAGG	1499 TGGGCAAGCTGTGCAAGCTGCTGGGCGCAAAGGCCCTGACCAACTGCTGCCCTGA 1	1559 4526 1619	4586 GCGTGTACTACGACCCCAGCAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCCAGGGCC 4	4646 AGTGGACCTACCAGAGCCCTTCAAGAACCTGAAGACGGCCAGAGGCCCC 4	4706 GCATGAAGGCCCCCACACCACGAGGCTGAAGCAGCTGACGAGGCCGTGCAGGCGTGAAGATCG 4	4766	4826 1919 4886	Qy 1979 GCGCCGAGACCTTCTACGTGGACGGCCGCCACCGCGAGCCGAGACCAAGATCGGCAAGGCCG 203 Db 4946 GCGCCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAAGACCAAGCTGGGCAAGGCCG 500	QY 2039 GCTACGTGACCGGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGCAGCAGCAGCAGCAGCAGCAGCAGC
Query Match 82.1%; Score 2027; DB 6; Length 12411; DB Best Local Similarity 91.6%; Pred. No. 2.6e-203; Indels 16; Gaps 4; DB Matches 2194; Conservative 0; Mismatches 185; Indels 16; Gaps 4; DB 14 TGGCCGAGGCCATGAGCAGGCCACCAGGGCCAACATCTGAACATGCAGCAGCAACT DB DB 2967 TGGCCAAGGCCAAGGGAAGACAGAGGCCACATCAACAGGGCCACATCACAAGAGGCCACATCACCAAGCGCAACAGCAGCCCAAGCGCAAGAGAGGCCCAAGCGCCC 130 DB 71 TCAAGGCCCCAAGCGCATCATCAACAGAGGCCACAAGAGAGCCCACATCGCC 130 DB 3027 TCCGCAACCACAGCAAAGAAGTGATTCAACTGCAGCAAGAGGCCCAACGCCC 3086 DB		CAAG 3205 (GAGC 310 (GAGC 3265	3325 418 3385	TGGGCGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGCCTGCTGCTGGAGG 478	479 AGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTTCATCA 538	539 AGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAGGCCATCGGCACCG 598	658 3625		3745 338		ACAACACCCCCTGTGTTCGCCATCAAGAAGAACAGCACCAAGTGGCGCAAGCTGGTGG 3865 ACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTCGGCATCCCC 958	3985

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Lian, Y., Hartog, K., Liu, H.,
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UP 2002533124-A/71
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30-DEC-1999 UP 2000591193
31-DEC-1998 US 60/114495,01-DEC-1999 US 60/168471 PI
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N HARTOG,
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CI2N15/09, A61K31/711, A61K38/00, A61K48/00, A61P31/18, A61P37/02,
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                                                                                                                                                                                                                                                                      PC C12N7/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC Description of Artificial Sequence: FS(-).protmod.RTopt.YM Location/Qualifiers
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Location/Qualifiers
1. 2306
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Pred. No. 6.1e-203;
0; Mismatches 138; Indels
other sequences; artificial sequences.

1 (bases 1 to 2306)
Barnett,S., Megede,J.Z., Srivastava,I., Liegreer,C., Selby,M. and Walker,C.
Improved expression of HIV polypeptides and virus-like particles
Patent: JP 2002533124-A 71 08-OCT-2002;
CHIRON CORP
OS Artificial Sequence
PN JP 2002533124-A/71
PP 30-OCT-2002
PF 30-DEC-1999 JP 2000591193
PR 31-DEC-1999 US 60/114495,01-DEC-1998
SUSAN BARNETY,JAN ZUR MEGEDE,INDRESH SRIVAS KARIN HARTOG,
PI HONG LIU,CATHERINE GREER,MARK SELBY,CF
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2306 bp DNA linear PAT 17-JUL-2003 HIV polypeptides and production of

BD263704
Improved expression of HI virus-like particles.
BD263704
BD263704.1 GI:33073472
JP 200253124-4A/71.
synthetic construct

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

LOCUS DEFINITION

RESULT 13 BD263704

AGAITCHACCOCCUS ACCECUTOTIC CONCINCTION	CCACCAACCAGAAGACCAGCTGCAGGCCATCC CCACCAACCAGAAGACCGAGGCCATCC CCACCACCAGAAGACCGAGGCCAGTCCCCAGAGGCCACTCCCCAGAGACCAGACCCCCAGATCACCCCCAGAGACCCCCCCAGATCACCCCCAGAGACCCCCCCAGATCATCGAGCCAGACCTGCAGACCTCCCCAGAGACCCCCCACAGATCATCGACCTGAGCCACAGACCTCCCACAGACCTCCTGAACCTCCCACAGACCTCCTCAGACCTCCCCCCCACAGGCATCCTCGAACCTCCCCACAGGCCATCCTCACAGCCCCCCCC	Query Match 82.0%; Score 2025.2; DB 6; Lo Best Local Similarity 93.3%; Pred. No. 6.1e-203;
0y 758 AGAAGATCAAGGCCCC 0b 601 AGAAGATCAAGGCCCCCAGA 0y 818 AGATCGCCCCCAGAAGC 0b 661 AGATCGGCCCCCAGAAGC 0y 878 CCAAGTGGCGCAAGC 0y 878 CCAAGTGGCGCAAGC 0y 878 CCAAGTGGCGCAAGC 0y 878 CCAAGTGGCGCAAGC 0y 101 AGATGCAGCTGGCAAGC 0y 998 TGGACGTGGCACCCCAGGCACC 0y 1058 TGGACGTGGCACCCCAGC 0y 1058 TGGACGTGGCACCCCCAGC 0y 1058 TGGACCTTCCCCAGCCCCCAGC 0y 1071 TGGACCTTCCCCAGCCTCGACC 0y 1071 TGGACCTTCCCCAGCCTCGACC 0y 1071 TGGACCTTCCGCCACCCCCAGC 0y 1075 TGGACCCTTCCGCCACCCCCCACCCCCCCCCCCCCCCCC	10 10 10 10 10 10 10 10	Db 1615 CCGAGGCCGTGCAGAAGGTGAGCACCGAGAGCATCGTGATCTGGGGCAAGATCCCCAAGT 1674

AACGCGCCCAACCGCG 2017 CGGCAGAAGATCGTGAGCC 2077 AGCTGGCCTGCAGGACA 2137 THE STATE OF THE S ARCAGCTGATCAAGAAGG 2257 GGGGCAACGAGCAGATCG 2317 ACGCATCGATGGCGGCA 2377 GGGGCCTAGGATCGATT 2437 CCGACTACTGGCAGGCCA 1897 inear PAT 13-SEP-2004 m, Y., Hartog, K., production of Length 2306; quence:

Qy 698 CCGTGAAGCTGAAGCCCGCATGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGG 757 Db 541 CCGTGAAGCTGAAGCCGGGATGGACGCCCCAAGGTCAAGCAGTGGCCCCTGCCGAGG 600 Qy 758 AGAAGATCAAGGCCCTGACCGCATCTGCGAGGAAGGAAGG	### ### ##############################
Qy 2318 ACAAGCTGGTGAGCAACCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCA 2377 Db 2155 ACAAGCTGGTGAGCGCCGCATCCGCAAGGTGTTCCTGAACGGCATCGATGGCGGCA 2214 Qy 2378 TCGTGATCTACCAGTACATGGACGTGTACGTGGCGGCGCGCCCTAGGATCGATT 2437 Db 2215 TCGTGATCTACCAGTACATGGACGTGTACGTGGGCGCGCGC	March 15

78 CCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGT 1837	15 ccgadgeccgrdcadaadgrgagcaccgadagcarcgrgarcrgggggaagarccccaagr 1674	38 TCGCCTGCCCATCCAGAAGGAGACCTGGGAGCCTGGTGGACCGACTACTGGCAGGCA	75 TCAAGCTGCCCATCCAGAAGGAGACCTGGGAGGCCTGGTGGATGGA	98 CCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCTGGTGAAGCTGTGCTACCAGC 1957	35 CCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGC 1794	58 TGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCG 2017	95 TGGAGAAGGAGCCCATCGTGGGCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCG 1854	18 AGACCAAGATCGGCAAGGCCGGCTACGTGACCGACGGGGCCGGCAGAAGATCGTGAGCC 2077	55 AGACCAAGCTGGGCTAGGCCGGCTACGTGACCGGGGCCGGGGGGTGGTGGTGGTGGGGGGG 1914	78 TGACCGAGACCACCAACCGAGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAGACA 2137	15 TCGCCGACACCACCACCAGAAGACCGAGCTGCTGCTTCTTCTTGGCCCTGCAGACA 1974	88 GCGGCAGCGAGCTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCC 2197	75 GCGGCCTGGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCC 2034	98 AGCCCGACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGG 2257	35 AGCCCGACAAGAGCGAGGGGAGCTGGTGAGCAGATCATCGAGCAGCTGATCAAGAAGG 2094	58 AGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGACGAGCAGCAGCAGCG 2317	35 AGAAGGTGTACCTGGCTGCCCGCCCAAAGGGCATCGGCGAACGAGCAGGTGG 2154	18 ACAAGCTGGTGAGCAAGGGTTCCGGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCA 2377	55 ACAAGCTGGTGAGCGCCGGCATCCGCAAGGTGCTGTTCCTGAACGGCATCGATGGCGGCA 2214	78 TCGTGATCTACCAGTACATGGACGTGCTACGTGGGCAGGGCGGCCCTAGGATCGATT 2437	15 TCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCGGCGGCGGCCCTAGGATCGATT 2274		75 AAAAGCTTCCCGGGGCTAGCACCGGTGAATTC 2306	
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PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Petentin Ver. 2.0
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| Sequence 45, Application US/10190435
| Publication No. US20030143248A1
| GENERAL INFORMATION:
| APPLICANT: ZUR MEGEDE, Jan
| APPLICANT: LIAN, Ying
| APPLICANT: LIAN, Ying
| APPLICANT: ENGELBRECHT, Susan
| APPLICANT: ENGELBRECHT, Susan
| APPLICANT: WAN RENSBURG, Estrelita J.
| TITLE OF INVENTION: POLYPEPTIDES PRODING ANTIGENIC HIV TYPE C
| TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
| FILE REFERENCE: PP18133.003 / 2302-18133
| CURRENT APPLICATION NUMBER: US/10/190,435
| CURRENT FILING DATE: 2002-12-30
| NUMBER OF SEQ ID NOS: 319
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: p2Polopt_C
US-10-190-435-45
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ORGANISM: Artificial Sequence
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Matches 2457; Conservative
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APPLICANT: LIAN, Ying
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC I
TITLE OF INVENTION: PPOLYNUCLEOTIDES, POLYPEPTIDES,
FILE REFERENCE: 2302-18702 / 18702.002
CURRENT APPLICATION NUMBER: US/10/190,305A
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 39
                                                                                                                    TYPE: DNA
ORGANISM: Artificial
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                                CTGTGCAAGCTGCTGCGCGCGCGCGAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG
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Sequence 39, Application US/10190305A Publication Wo. US20030198621A1 GAPERAL INFORMATION: APPLICANT: ZUR MEGEDE, Jan

1861	RESULT 4 19.09-09.59-575-31 19.09-09.59-575-31 19.09-09.50-575-31 19.09-09.50-575-31 19.09-09.50-575-31 19.09-09.50-575-31 19.09-09.50-575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.575-31 19.09-09.59-12-30 19.09-09.59-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 19.09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-12-30 20.00-09-09-09-12-30 20.00-09-09-12-30 20.00-09-09-09-12-30 20.00-09-09-09-12-30 20.00-09-09-09-12-30 20.00-09-09-09-09-09-09-09-09-09-09-09-09-0
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                  GGCACCCTGAACTTCCCCCCAGATCACCCTGTGGCGCCCCCCTGGTGAGGTG
                                                        GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGACGACGACGAGGAG
                                                                                 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGCTTCATCAAG
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                                                           CCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATC
                                                                                             CGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGAC
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                                                                                                                                                                                                                                                                                             Sequence 44, Application US/10190435

Publication No US20030143248A1

GENERAL INFORMATION:

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: BARNETT, Susan W.

APPLICANT: BARNETT, Susan W.

APPLICANT: BRIGELBRECHT, Susan

APPLICANT: PROFEINER SUSAN

APPLICANT: PROFEINER SUSAN

APPLICANT: PANTIGENECHT, Susan

APPLICANT: PANTIGENECHT, Susan

APPLICANT: VAN RENSBURG, Estrelita J.

TITLE OF INVERTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: PP18133.003 / 2302-18133

CURRENT APPLICATION NUMBER: US/10/190,435

CURRENT PILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 319

CONTRAINT APPLICATION VET. 2.0
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ORGANISM: Artificial Sequence
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LENGTH: 2457
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; Sequence 38, Application US/10190305A
; Publication No. US20030198621A1
; CENERAL INFORMATION:
    APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
; WURBER OF SEQ ID NOS: 93
; SEQ ID NO 38
; LENGTH: 2457
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98.6%; Score 2434.6;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2453; Conservative 0; Mismatches
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19-899-575-32 97.8%; Score 2415.4; DB 10; Length 2457; Secore 2415.4; DB 10; Length 2457; Secore 2415.4; DB 10; Length 2457; Secore 2451; Conservative 0; Mismatches 6; Indels 12; Gaps Greacgecaccargaccaaggecargacaaggecacaggecacaggecacaggecacaggecacaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecaggecagg	PACTICAAGGGCCCAAGGGCAICAICAAGIGCIITCAACIGGGGGAAGG 		TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACGGCCCAACGCCCAAGGCCAGCAGC	301 AGCCGCGAGCTGCAGGTGCGCGGCGAACCCCCGCAGCGAGCCGGCGCGGCGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGCAGGCGAGGCGGAGGCGGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCAAGCCCCGGAGGCAAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCAAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCAAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGAG	361 GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTG	421 GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACGTGCTGGAGGAG 	481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTCGGCGGCTTCATCAAG	541 GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGCCATCGGCACCGTG	601 CTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGCTG	661 ACCCTGAACTTCCCGATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG	721 GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACGCCCCTGACGCCCTGACGGAGAGATCAAGGCCCTGACGCCCTGACCGAGGAAGATCAAGGCCCTGACCGCCCTGACCAAGAAAGA	781 ATCTGCGAGGAGTGGAGAGAGGGCAAGATCACCAAGATCGCCCGAGAACCCCTAC		TTCCGCGAGCTGAACAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCC 	961 CCGGCCGGCCTGAAGAAGAAGAGGGTGACCGTGCTGGACGTGGGGGACGCCTACTTC

247 CAGGGCAAGGCCCGCAGTTCCCCAGCAGAACCGGCCAACAGCCCCACCAGCCGC 306 241 CAGGGCAAGGCCCGCAGTTCCCCAGCAGACACACCCCACCACCAGCCGC 306 241 CAGGGCAAGGCCCGCAGAGTTCCCCAGCAGACACACACAC	667 AACTTCCCCATCAGCCCATCGAACCGTGCCCTGAAGCTGAAGCCGCATCGACGC 726 661 AACTTCCCCATCAGCCCCATCGAACCGTGCCCGTGAAGCCGCATCGACGC 720 727 CCCAAGGTGAAGCAGTGCCCCTGACCGCGCATCGACGCC 720 728 CCCAAGGTGAAGCAGTGCCCCTGACCGGCATCTGC 786 729 CCCCAAGATGAAGAAGATGCCCCTGACCGGCATCTGC 786 731 GAGGAGTGAAGAAGATGCCCCTGACCGAGAAGCTCAACACCC 846 731 GAGGAGTGAAGAAGAAGAAGAACACACAAGTTCGCCCCGAAACCCTTACAACAC 840 847 CCCCTGATTCCCCATCAAAAAAAAAAAAAAAAAAAAAAA
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	RESULT 9 US-10-190-305A-37 i Sequence 37, Application US/10190305A j Publication No. US20030198621A1 general information: APPLICANT: ZUR MEGEDE, Jan j APPLICANT: BARNETT, Susan j APPLICANT: LIAN, Ying TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF		; SEQ ID NO 37 ; LENGTH: 2445 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE:	S-1	Query Match 97.3%; Score 2401.8; DB 16; Length 2445; Best Local Similarity 99.2%; Pred. No. 0; Matches 2438; Conservative 0; Mismatches 7; Indels 12; Gaps	Oy 7 GCCACCATGGCCATGAGCCAGGCCACCAGGGCCAACATCCTGATGCAGGGCAGC 66	QY 67 PACTICAAGGGCCCAAGCGCATCAICAAGTGCTTCAACTGCGGCAAGGAGGCCACAIC 126	Oy 127 GCCGCAACTGCCGCGCACACAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCAC 186	0y 187 CAGATGAACTGCACCGAGGCCAACTTCTTCGCGAGGACCTGGCCTTCCCC 246	OY 247 CAGGGCAAGTTCCCCAGGAGCAAACCGGGCCAACAGCCCCACCAGCCGG 306	OY 307 GAGCTGCAGGCGCGCAAACCCCCGCAGCGAGCGGCGCCGAGCGCCAGGGCACCCCCC	Oy 367 CTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGC 4.26	QY 427 CAGATCAAGGAGCCCTGCTGGACACCGCGCCGACGACACCGTGCTGGAGGAGATGAGC 486 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 487 CTGCCCGGCDAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGC 546 L	QY 547 CAGTACGACTCCTGATCGAGATCTGCGGCAAGAAGCCATCGGCACCTGCTGATC 606	dy GGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGGCTGCACCTG 666
1327 AAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAG 1386	TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAG	1489 CTGTGCAAGCTGCGCGGGGCGCCAAGGCCCTGACCGACGTCGTGCCCCTGACCGAGGAG 1548 1567 GCCGAGCTGGCCGAGAACCGCGAGATCCTGCGGGGGCCCGTGCACGGCTGTAC 1626	1627 TACCACCCCAGCAAGCACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGGACC 1686 	1687 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGCAAGTACGCCAAGATGCGC 1746 	1747 ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCCTGCAGAAGATCGCCATGGAG 1806 	1807 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG 1866	1867 GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCGAGTGGGAGTTCGTGAAC 1926 	1927 ACCCCCCCTGGTGAAGTTGTGGTACCAGCTGGAAAGGAGCCCATCATCGGCGCCGAG 1986 	1987 ACCTTCTACGTGGACGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG 2046	2047 ACCGACCGGGGGGGGGGAGAAGATCGTGACCTGACCGACACCACCAACCA	2107 CTGCAGGCCATCCAGCTGGCCCTGCAGACAGCGGCAGCGAGGTGAACATCGTGACCGAC 2166	2167 AGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCAACAAGAGCGAGAGCGAGTGGTG 2226 	2227 AACCAGATCATCGAGCAGCTGATCAAGAAGAGAGAGGTGTACCTGAGCTGGGTGCCGGCC 2286 	2287 CACAAGGGCATCGGCGGCAACGAGATCGACAAGCTGGTGAGAGGGAGCGTCCGCAAG 2346 	2347 GTGCTGTTCCTGGACGGCATCGATGGCGCGATCGTGATCTACCAGTACATGGACGACCTG 2406 	07 TACGIGGGCAGCGGCCCTAGGAICGATTAAAAGCTICCCGGGGCTAGCACCGGT 246

1949 TACCAGANCCACCAAGGACCCTTCAAGAACCTGAAGACCTCCACACACTACGCCCAACACTCCCCACACCACCACCACCACCACCACCACCA	RESULT 10 US-10-190-435-9 i Sequence 9, Application US/10190435 j Sequence 9, Application WS/10190435 j Publication No. US2003014324841 j GENERAL INFORMATION: j APPLICANT: ZUR MEGENE, Jan j APPLICANT: BARNET; Susan W. j TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C j TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF j TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF j TITLE OF INVENTION NUMBER: US/10/190, 435 j CURRENT PLING DATE: 2002-12-30 j NUMBER OF SEQ ID NOS: 319 j SOFTWARE: Patentin Ver. 2.0 j SEQ ID NO 9 j LENGTH: 3930 j TYPE: DNA j CREANISM: Artificial Sequence j FEATURE:
601 GGCCCCCCCCGGGAACATCATCGGCCGCAACATGCTGAACCTGGGCTGGCT	1387 TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGAGAGCTGGACCGTGAACGACATCCAG

AGAAGAAGAGAGCGTGACCGTGCTGGACGACGCCTACTTCAGCGTGCCCCTGG 25 ACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAAGAGACCCCCG 10 ACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCG 25 ACGAGGACTTCCGCTACCAGTGCTGCCCCAGCATCCAGCATCAACAACGAGACCCCCG 25 GCATCCGCTACCAGTACAACGTGCTGCCCCAGGGTGGAAGGGCAGCCCCAGCATCTTCC 11 GCATCCGCTACCAGTACAACGTGCTGCCCCAGGGTGGAAGGGCAGCCCCAGCATCTTCC 26 AGAGCAACACAACATCCAGAGCTGCTCCCCAGGGTGCAACCCCAGCATCTTCC 26 AGAGCAACACACACAACATCCAGAGCTGCCCCCAGGATCGTGATCT 26 AGAGCACACACACACACACACCTCCCCGCGCCCCCAGATCGTGATCT 26 AGAGCACACACACACACACACCCCAGAGCCCCCAGATCGTGATCT 26 AGAGCACACACACACACACACACCCCAGAATCGTGATCT 26	1214 ACCAGTACATGGACCACCTGTACGTGGACCTGAGAATCGGCCACCACCACCACACA 1273 2687 ACCAGGCCCCCTGTACGTGGGCGGCGCGCGGCGCCACCACGCGCCCA 2740 1274 AGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGGGGCTTCACCACCCCCGACAAGAAGC 1333 2741 AGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGGGCTTCACCACCCCCGACAAGAAGC 2800 1334 AGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGGGCTTCACCACCCCCGACAAGAAGC 2800	01 ACCAGAAGGAGCCCCCCTTCCTGCCCATCGAGCTGCACCGCGACAAGTGGACCG 28 94 TGCAGCCCATCGAGCTGCCCGAAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGG 14 95 TGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGAAC	15 TGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCGGGCATCAAGGTGCGCCAGCTGTGCA 297 14 AGCTGCTGCGGGGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGG 15 AGCTGCTGCGGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGG 16 AGCTGCTGCGCGGCGCCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGG 17 AGCTGCTGCGCGGCGCCCAAGGCCCTGACCGACCATCGTGCCCTGACCGAGGAGGCCGAGG 18 AGCTGCTGCGCGGCGCCCAAGGCCCTGACCGACCATCGTGCCCTGACCGAGGAGGCCGAGGC 19 AGCTGCTGCTGCCGAAGGCCCTGACCGACCATCGTGCCCTGACCGAGGAGGCCGAGGC 10 AGCTGCTGCTGCCCTAACCGACCAACGCCTGACCGACGCCGAGGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGCCGAGGAG	1574 TGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACC 1633	694 T 155 T 754 A 215 A	187 333 193 339	1934 CCCTGGTGAAGCTGTGGTGAAGAAGCCCATCATCGGGGCCGAGACCTTCT 1993
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<pre> ; OTHER INFORMATION: Description of Artificial Sequence: GagComplPolmut_C US-10-190-435-9 Query Match Query Match Best Local Similarity 99.2%; Pred. No. 0; Matches 2431; Conservative 0; Mismatches 7; Indels 12; Gaps 2; Qy</pre>	Qy 134 ACTGCCGCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGCCACCAGATGA 193 Db 1607 ACTGCCGCGCCCCCGGAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCACCAGATGA 1666 Qy 194 AGGACTGCACGCCCCAGGCCAACTTCTTCCGCGAGGACTTCCTCCCCAGGGCA 253 Db 1667 AGGACTGCACGAGGCCAACTTCTTCCGCGAGGACTTCCTCCCCAGGGCA 253	Oy 254 AGCCCGCGGAGTTCCCCAGGGAGCAGAACCGCGCCACCACCAGCCGCGGGGGCTGC 313 Db 1727 AGCCCGCGGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGC 1786 Oy 314 AGCTGCGCGCGAACAACCCCCGAGCGGCGCGCGAGCCCCAGGCCACCCTGAACT 373 Db 1787 AGCTGCGCGGCGAACAACCCCCGCAGGCCGAGCCCCAGGCCCCTGAACT 1846	374 TCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 43 1847 TCCCCCAGATCACCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 19 434 AGGAGGCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 19	TACG 55 TACG 20 TACG 20	2027 ACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCA 614 CCCCCGTGAACATCGTCGGCCGCAACATGCTGACCCGAGCTGGGCTGCACCTGAACTTCC	0 0-0 0-0	### ### ##############################

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1727 AGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCAACAGCCCCACCAGCCGCGGGGGTGC 1786
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                                               AGGTGCGCGCGACAACCCCCGCAGCGAGGCCGGCCCGAGCGCCCAGGGCACTCTGAACT
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                                                                                                                                                                        AGGAGGCCCTGCTGGACTCCGGCGCCGACACCGTGCTGGAGGAGATGAGCCTGCCCG
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US-10-190-435-10
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; Sequence 10, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICAMT: EARNETT, Susan W.
; APPLICAMT: EARNETT, Susan W.
; APPLICAMT: LIAN, Ying
APPLICAMT: LIAN, Ying
APPLICAMT: WAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYVPLETIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYVPLETIDES, POLYPEPTIDES AND USES THEREOF
; TITLE OF INVENTION: POLYVPLETIDES, POLYPEPTIDES
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT PILING DATE: 2002-12-30
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3930
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ORGANISM: Artificial Sequence
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                                                                 GENERAL INCARATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: EARNETT, Susan W.
APPLICANT: LIAN, Yang
APPLICANT: WELSBERCHT, Susan
APPLICANT: WESTERRECHT, Susan
TITLE OF INVENTION: POLYMUCLEOTIDES, BOLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYMUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: NOWHER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SEQ ID NOS: 319
SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                 DB 15; Length 3930,
                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
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Best Local Similarity 99.2%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches
                           ; Sequence 11, Application US/10190435; Publication No. US20030143248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
RESULT 12
US-10-190-435-11
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 TGCAGCCCATCGAGCTGCCCGAGAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGG
                                                         TGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCCAGCTGTGCA
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1754 ACACCANCGACGTGAACCAGGCCGTGCAGAACATCCCCATGGAACACGTCGTGGAACATCGCTGAACATCGCTTGGAACATCGCTTGGAACATCGCCTTGGAACATCGCCTTGGAACAACCCTTGGAACAACATCGCCTTGGAACAACCCTTGGAACAACCTTGGAACAACCCTTGGAACAACCCTTGGAACAACCCTTGGAACAACCCTTGGAACAACCCTTGGAACAACCTTGGAACAACCTTGGAACAACCCTTGGAACAACCTTGGAACAACCCTCAACAACAACCCCCCAACCAA	RESULT 13 US-10-190-435-58 is Sequence 58, Application US/10190435 is Sequence 58, Application No. US20030143248A1 is Publication No. US20030143248A1 is Publication No. US20030143248A1 is Publication No. US20030143248A1 is APPLICANT: ZUR MEGEDE, Jan is APPLICANT: ENGELBRECHT, Susan W. is APPLICANT: PROBREMENCE BYLOGING ANTIGENIC HIV TYPE C it TITLE OF INVENTION: POLYPERIDES ENCODING ANTIGENIC HIV TYPE C it TITLE OF INVENTION: POLYPERIDES POLYPERTIDES AND USES THEREOF is TITLE OF INVENTION: POLYPERIDES. is CURRENT APPLICATION NUMBER: US/10/190,435 is CURRENT FILING DATE: 2002-12-30 is NUMBER OF SEQ ID NOS: 319 is SOFTWARE: Patentin Ver. 2.0 is SEQ ID NO 58 is LENGTH: 5184 is TYPE: DNA is ORGANISM: Artificial Sequence is FRATURE: is OTHER INFORMATION: Description of Artificial Sequence: TatRevNefgagCpolIna C US-10-190-435-58
674 CCATCAGGCCCCATCAGGACCGTCAAAGCTGAAGCCCGCATTGAACGCCCCAAGG 2147 CCATCAGGCCCCATCCAGGACCGTCAAAGCTGAAGCCCGCCATTGAAGCCCCCAAGG 2147 CCATCAGGCCCCATCCAGGACCGTCACCGCTGAACGCCCCCAAGGCCCCCAAGG 2207 TGAAGCAGTGGCCCCTGACCGAGAAGAACTCAAGCCCCTGACCGCCATTGCCGCAGGAG 2207 TGAAGCAGTGGCCCCTGACCGAGAAGAACTCAAGCCCTGACCGCCATTGCCGCAGGAG 2207 TGAAGCAGGCCCTGACCGCAGAAGAACTCAGCCCTGACCGCCATTGCCGCAGCAGG 2207 TGAAGAAGGAGGCCCTGACCAGAACTCAGCCCCTGACCCCCTGACCCCCTGACCCCCTGTGTG 2217 TGGCAAAGAAGGAGAACACACCACAACTCGCCCCCGAGAACCCCTCAACACCCCCGGTTG 2227 TGGCAACAAGAAGAAGAACAACACCCCCAACACTCGCCCCTGACACCCCCCGGTTG 2227 TGGCACCTCAAGAAGAAGAACACTCACCAACACCCCCCAGAACCCCCTCAACACCCCCCGGTTG 2227 TGGCACCTCAAGAAGAAGAACACTCACCAAGTCGCCCCTGAACACCCCCCCC	1394 TGCAGCCCATCGAGCCGAGAAGGAGACCGTGAACGACATCCAGAAGCTGG 1453

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2174 ACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCCAGGCGAGCTGGTGAACCAGA 2233	è 8	374 TCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 433
2234 TCATCGAGCAGCTGATCAAGAAGAAGAGGTGTACCTGAGCTGGGTGCCCGCCC	& g	434 AGGAGGCCTGCTGGACACCGGGCCGACGACGACGACGAGGAGGAGATGAGCCTGCCCG 493
2294 GCATCGCCGCCACCACACCACATCGACAAGCTGGTGAAGGGCATCCGCAAGGTGCTGT 2353	& g	494 GCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACG 553
2354 TCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGACTGTACGTGG 2413 	& g	554 ACCAGATCCTGATCGAGATCTGCGGGAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCA 613
2414 GCAGCGGCCCTAGGATTAAAAGCTTCCCGGGGTAGCACCGGT 2463 	& 8. 	614 CCCCCGTGAACATCATCGGCCGCAACATGCTGACCCGGGGGTGGGCTGCACCTGAACTTCC 673
ULT 14 10-190-305A-82	& 8	674 CCATCAGCCCCATCAGACCGTGAAGCTGAAGCTGGACGGCATGGACGCCCCAAGG 733
- G	& 8	734 TGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGGA 793
APPLICANT: LIAN, Ying TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF	ራ ብ	794 TGGAGAAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGT 853
FILE REFERENCE: 23-18/02 / 18/02.002 CURRENT PILING DATE: 2002-07-05 NUMBER OF SEQ ID NOS: 93	& 8	854 TCGCCATCAAGAAGAAGGACACCAAGTGGCGCAAGCTGGTGGTGGACTTCCGCGAGCTGA 913
SOFINE: Facellin ver. 2.0 LENGTH: 5184 TYPE: DNA	, , 8 &	914 ACAAGCGCACCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGGCCGG
ONGARIANS ALLILLIA SEQUENCE PEATURE: OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: TatRevNefgagCpolina C	<u>ک</u> و	974 AGAAGAAGAGAGGGTGACCGTGCTGGACGTGGCGCGACGCCTACTTCAGCGTGCCCTGG 1033
96.9%; Score 2393.2; DB 16; Length 5184; larity 99.2%; Pred. No. 0;	S G	1034 ACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCG 1093
o; minuaccines o; indeis AGCCACCAGCGACATCTGATGCAGCGG AGCCCACCAGCGCGAACATCTGATGCAGCGG AGCCAACAACATCTGATGCAGCGGAACAACATCTACAACAACAACAACAACAACAACAACAACA	, B &	1094 GCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCC 1153
S CCCC	상 염	1154 AGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCT 1213
2801 MGGGCCCCCCGGAGCAGCTGCTGCGGCGAAGGGCCCCACATCGCGCCCGCA	상 옵	1214 ACCAGTACATGGACGACCTGTACGTGGGCGACCTGGAGATCGGCCAGCACCGCCCA 1273
AGGACTGCACCGCCCACCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGA AGGACTGCACCGGGGCCAACTTCTTCCGCGAGGACCTTCGCCCTTCCCCCAGGGCA	ò a	1274 AGATCGAGGAGCTGCGCAAGCACCTGCTGCGGTGGGGCTTCACCACCCCCGACAAGAAGC 13333
AGGCCGCGAGTTCCCCAGCGAGCAGCAACAGCCCCAACAGCCCCACCAGCGGGGCTGC	& g	1334 ACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCGACAAGTGGACCG 1393
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1814 TGATTCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCTCCCAAGACCTGGGGAACCTT 2335 2876 TGATTCTGGGGCAAGACCCCCAAGTTCCGCTGGCCTGCCAGACCTGGGAACCTCT 2335 2876 TGATTCTGGGCACTACTGGGAACCTCGAATCCCCAAGTGGGAACCTCCCCC 2335 2876 GGTGGACCGACTACTGGCAGCCCACTGGAACTCCCCAAGTGGGAACTCGTGAACACCCCCC 2395 2876 GGTGGACCGACTACTGGCAGCCCACTGGAACTGCGCAGACCTCCCC 2395 2876 CCCTGGTGAAGACTGTGGAACCTTGGAACACCCCCAATCATGGGGCCCAGAACTTCT 1395 2876 CCCTGGTGAAGACTGTGGAACCTTGAAGACCCATCATGGGCCCAGAACTTCT 1395 2876 ACGTGGACCGCCCCCAACCGCGGAACCCAACACCCCCACCACCA	Search completed: June 2, 2005, 04:23:32 Job time : 1424.77 secs
1748 CCATCAGCCCCATCGAGCCGTGAAGCTCAAAGCCCGCATGGAGCGCCCAAGG 1807 1818 CCATCAGCCCCATCCGAGCGAAACCTCAAGCCCCGACTCGCGCGAGGAGA 1918 1818 TGAAGCAGTGGCCCCTGACCGGGAAAATCAGGCCCCTACCGCCCATCTGCGGGGAGA 1867 1819 TGAAGAAGGAGGCCAAGATCACCCAAGAACCCCTTGCAACACCCCCTTG 1921 1819 TGGCATCAAGAAGAACACCAAGATCGGCCCCGAAAACCCCTACACACCCCCGTTG 1927 1819 TGGCATCAAGAAGAACACACCAAGATGGCCCCGGAAACCCCTACACACCCCCTTG 1927 1819 TGGCATCAAGAAGAACACACCCAAGATGGCCCCGGAAACCCTTCAACACCCCTTCA 1987 1810 TGGCATCAAGAAGAACACACCCAAGATGGCCCCGCAACACCCCCCCC	1394 TGCAGCCCATCGAGCAGAAGGAGGCCGTGAACGACATCCAGAAGCTGG 1453 2456 TGCAGCCCATCGAGCTGCCCGAGAAGCTGGACCGTGAACCTCCAGAAGCTGG 2515 1454 TGGGCAAGCTGCACCCGAGAAGCTGCACCCGCATCAAGCTGCCCAGCTGTGG 2515 1514 TGGGCAAGCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTGCCCAGCTGTGCA 1513 2516 TGGGCAAGCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTGCCCAGCTGTGCA 2575 1514 AGCTGCTGCGCGCCAAGGCCCTGACCGACATCATGCCCCTGACCGAGGAGCCCGAGCTGTGCC 2635 1574 TGGAGCTGGCGCCCAAGGCCCTGACCGACATCATGCCCCTGACCGAGGAGCCCGAGC 2635 1574 TGGAGCTGGCCGAGAACCGCGAGATCCTGCGCAGCACCGAGGAGCCCAAGCCCAGCCGAGCCCGAGCCCGAGGAG

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Sequence 11, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 14, Appl Sequence 11, Appl Sequence 11, Appl Sequence 13, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl 10, Sequence 11, Appl 10, Sequence 11, Appl 11, Sequence 11, Appl	ANTIGENIC HIV TYPE C DES AND USES THEREOF	imilarity 100.0%; Score 2463; DB 10; Length 2463; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0 GTCGACGCCACCATGGCCGAGGCCATGAGCCACCACGCCCACATCCTGATGCAG 60 GTCGACGCCACCATGAGCCATGAGCCACCACGCCACACATCCTGATGCAG 60 GTCGACGCCACCATGAGCCACCACACACGCCAACATCAGCGAGCACACACA
5 US-10-190-435-11 5 US-10-190-435-13 6 US-10-190-435-13 5 US-10-190-435-13 5 US-10-190-435-13 6 US-10-190-435-15 6 US-10-190-435-15 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-435-40 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-190-305A-31 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13 6 US-10-241-009-13	ALIGNMENTS 75 18 Janse 25 ENCODING POLYPEPTII 899,575 704	100.0%; Score 2463; DB 10; Lengt imilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels GrGGAGGCCATGAGCCAGGCCACGAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGAGCCAAGGCCAAGGCCAAGAGCCAAGGCCAAGAGCCAA
98 99 99 99 99 99 99 99 99 99 99 99 99 9	ALI. 109-899-575-31 209-899-575-31 209-899-575-31 209-899-575-31 209-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31 200-899-575-31	Similarity 100.0% 3; Conservative GTCGACGCCACCATGCCC
112 113 114 115 116 117 128 118 129 119 123 133 134 135 136 137 138 138 139 139 139 130 131 131 131 131 131 131 131	RESULT 1 US-09-899-575-31 Sequence 31, Applicat Publication No. US200 GENERAL INFORMATION: APPLICANT: Barnett, APPLICANT: Barnett, APPLICANT: BARNET, TITLE OF INVENTION: TITLE OF INVENTION: FILE REPERENCE: PPOI CURRENT APPLICATION FILE REPERENCE: PPOI CURRENT FILING DATE: PRIOR PILING DATE: PRIOR PILING DATE: NUMBER OF SEQ ID NOS SOFTWARE: PATENTIN INFORMATION: SEQ ID NO 31 LENGTH: 2463 TYPE: DNA ORGANISM: Artificia CHER INFORMATION: US-09-899-575-31	Query Match Best Local Sin Matches 2463; Qy 1 G7

6. COCROCOMMENTO MORPOSCOCIONO MORPOSCOTI MONTOCOTICO MORPOSCOTI 120 6. COLORO MORPOSCOCIONO MORPOSCOTI MONTOCOTICO MORPOSCOTI 120 6. COLORO MORPOSCOCIONO MORPOSCOTI MORPOSCOTI MORPOSCOTI 120 6. COLORO MORPOSCOTI MORP		1261 CGGCCGAAGATCGAGGACTGCTGCGGTGGGGGTTCACCACCCCGAC 1320	TGGACCGTGCAGCCCATCGAGCTGCCCGAGAGGAGGAGCTGGACCGTGAACGCCGTCAACGCCGTCAACGACGTCAACGACGTCAACGACGTCAACGACGTCAACGACGTCAACGACGAGAGCAGCTGCCCAGGAGAGGAGAGCTGGAACGTCGAACGTCAACGAGAGAGA	1441 AAGTIGGTGGGCAAGCTGAACTGGGCCAGATCTACCCGGGATCAAGGTGGCCCAG 1500 1441 AAGTIGGTGGGCAACTGAACTGGGCCAGAATCTACCCCGGCATCAAGGTGCCCCAG 1500 1501 CTGTGCAAGCTGGCGGGGGGCGGGCCGAAGGCCCGAAGGTGGGCCCTGACCGAGGAG 1500 1501 CTGTGCAAGCTGCTGCGGGGGGGGCGGGGCCTAACGTGCCCTGACCGAGGAG 1560	1501 CTGTGCAAGCTGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGGG 1560 1561 GCCGAGCTGCAGCTGGCGGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTAC 1620	1621 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC 1680 1621 TACGACCGAGCAAGCACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGACCAGGACC 1680	TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGCAAGTACGCCAAGATGCGC 	ACCGCCCACACCACCACGTGAAGCACTGACCGAGGCCGTGCAGAAGATCGCCATGGAG [AGCATCGTGATCTGGGGGAAGACCCCCAGTTCGGCTGCCCTGCGATCGGAAGGAGAGACTGG 	GAGACCIGGIGGACCCAACIACIGGCAGGCCACCIGGAICCCCGAGIGGGAGITCGIGGAAC 	ACCCCCCCTGGTGAAGCTGTGGTACAGCTGGAGAAGGAGCCCATCATCATCGGCCCAGG	ACCTTCTACGTGGACGCCGCCGCCGCGAAACCAAGATCGGCAAGGCCGGCTACTG	ACCGACCGGGGGCGGAGAACGTCAGCCTGACCGAGACCACCAACCA		2161 AGCCAGTACGCCCTGGGCATCATCCAGGCCCGACAAGAGCGAGAGCGAGC	2221 AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAGGTGTACCTGAGCTGGGTGCCGCC 2280
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CC CCCAC 960 ||||| |CCCAC 960 |||| |GGTG 420

1921 ACCCCCCCCTGGTGGAGCTGGTGGGAGCCCCTGGATCGCGGGGAGTTCGTGAAC 1920 1921 ACCCCCCCCTGGTGGAGCTGGTGGCCCCTGGATCGCGGCGCGGGGGGGG	RESULT 4 US-09-09-99-575-30 Sequence 30, Application US/09899575 Publication No. US20030223961A1 Sequence 30, Application US/09899575 Publication No. US20030223961A1 APPLICANT: Barnetk, Susan W. APPLICANT: Barnetk, Susan W. APPLICANT: Barnetk, Susan W. APPLICANT: Barnetk, Susan W. APPLICANT: WAS Renearly Bestreilta Janse TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C TITLE OF INVENTION: POLYMUCLEOTIDES POLYPEPTIDES AND USES THEREOF TITLE OF INVENTION: POLYMUCLEOTIDES, POLYPEPTIDES AND USES THEREOF TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF FRICK APPLICATION NUMBER: 09/475, 704 PRIOR APPLICATION NUMBER: 09/475, 704 PRIOR TILING DATE: 1999-13-30 SEQ ID NO 30 LENGTH: 2469 TTYPE: DNA TYPE: DNA TYP
	1381 TGGACCGTGCATCGAGCTCCCGAGAAGGAGCTGCCGTGAACCACTCCGG 140 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181 1181

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TGGGTG 2280 TGGGTG 2334 GGCATC 2334 GGCATC 2340 CATGGAC 2394 CATGGAC 2400 CATGGAC 2460 TAGCACC 2454 IMINIMATERIAL INGCACC 2460	APPLICANT: Barnett, Susan W. APPLICANT: Equalbrecht, Susan W. TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF C TITLE OF INVENTION NUMBER: US/09/899,575 CURRENT PEDLICATION NUMBER: US/09/899,575 CURRENT FILING DATE: 1999-12-30 FRIOR APPLICATION WUMBER: 09/475,704 FRIOR FILING DATE: 1999-12-30 NUMBER OF SEQ ID NOS: 135 SOFTWARE: Patentin Ver. 2.0 TENGTH: 2457 TYPE: DNA	Score 2436.2; DB 10; Length 2457; Pred. No. 0; O; Mismatches	301 AGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCGCAGGCGGCGGGCG

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241 CAGGGCAAGGCCCGCGAGTTCCCCAGCGGCGGAACCGCGCCCACCACCACCAGCCGC
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                                                                  APPLICANT: ZUR MEGEDE, Jan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: WAN RENBURG, Estrelita J.
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 2457
                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: p2Polopt_C
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                          Sequence 45, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
RESULT 6
US-10-190-435-45
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1795 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG 1854
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Db 1741 ACGCCCACACCAACGACGTGAAGAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG 1800	QY 1801 AGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG 1860	OY 1861 GAGACCTGGTGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1920	OY 1921 ACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG 1980 Db 1921 ACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG 1980	1981 ACCTTCTACGTGGACGCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG	Oy 2041 ACCGACCGGGCCGGCAGAAGATCGTGAGCTGACCGAGACCACCAGAGGCGGG 2100	Oy 2101 CTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGAGGTGAACATGGTGACGAC 2160	OY 2161 AGCCAGTACGCCTGGGCATCAGGCCCAGCCCGACAAGAGCCAGGCGGTGGTG 2220	OY 2221 AACCAGATCATCGAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC 2280	Qy 2281 CACAAGGGCATCGGCGGCAACGAGCAGAAGCTGGTGAGCAAGGCCATCCGCAAG 2340	GTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGACC 	QY 2401 TACGTGGGCGGCGGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACGGT 2457 DS 2401 TACGTGGGCGGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACGGT 2457	RESULT 7 US-10-190-305A-39 ; Sequence 39, Application US/10190305A ; Entering transformation US/10190305A	; GENERAL INFORMATION: ; APPLICANT: ZUR MEGEDE, Jan ; APPLICANT: BANNETT, Sugan	TITLE OF INVENTION: TYPE C POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF; FILE REPRENCE: 2302-18702 / 18702.002		; SEQ ID NO 55; ; TYPE: DNA ; ORGANISM: Artificial Sequence	; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: p2Polopt_C US-10-190-305A-39	Query Match 98.7%; Score 2430.2; DB 16; Length 2457; Best Local Similarity 99.6%; Pred. No. 0;
667 AACTICCCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCCGGCATGGACGGC 726	CCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAACATCAAGGCCCTGACGCCATCTGC	GAGGAGATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCTACAACACCCTACAACACCCTACAAAAACACCAAAAAA	CCGTGTTCGCCATCAAGAAGAAGCACCAGTGGCGCAAGTGGCTGGTGGACTTCCGC	907 GAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTCCCCCCACCCCGCC 966 	967 GGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGACGCTACTTCAGGGTG 1026 	1027 CCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACGAG 1086 	1087 ACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGC 1146	ATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCGCCGCAACCCCGAGATC	GTGATCTACCAGCCCCCCTGTACGTGGGCAGCGACGTGGAGATCGGCCAGCACACGAGATCTACAGATCACAGAGATCTACAGATCAGACAGA	25252 - - - 25252	1321 AAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCGGACAAG 1380 	1381 TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGAACCGTGAACGACATCCAG 1440 	1441 AAGCTGGTGGCCAAGCTGAACTGGGCCAGCCAGCTCTACCCCGGCATCAAGGTGCGCCAG 1500 	1501 CTGTGCAAGCTGCTGCGGGGCGCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG 1560	1561 GCCGAGCTGGAGCTGGCCGAGAACCCGGAGATCCTGGGGGGAGCCCGTGCAGCGGGGTGTAC 1620	1621 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGGCAGGGCCACGACCAGTGGACC 1680 1621 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGGAGGCCACGACAGTGGACC 1680	1681 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACGGGCAAGTAGGCCAAGATGGGC 1740 	1 ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG

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US-10-190-435-43
                                                                                                   CACAAGGGCATCGGGGAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCGGAAG
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AGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCGAGGCTGGTG
            AACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAAGGAGGGCCACATC
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; Sequence 43, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICAMT: ZUR MEGEDE, Jan
; APPLICAMT: BARNETT, Susan W.
; APPLICAMT: LIAN, Ying
APPLICAMT: LIAN, Ying
; APPLICAMT: VAN RENSBURG, Estrelita J.
; APPLICAMT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REPERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT PILING DATE: 2002-12-30
; SEQ ID NOS: 319
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 43
...LENGTH: 2445
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98.4%; Score 2422.6;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2441; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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US-10-190-305A-37; Sequence 37, Application US/10190305A; Publication No. US20030198621A1

1847 TCCCCCAGATCACCCTGTGGCAGCCCCCTGGTGAGCTCAAGGTGGCGGCCAGATCA 1906	Qy 674 CCATCAGCCCCATCGAGACCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG 733 Db 2147 CCATCAGCCCCATCGAGACCGTGCCCGTGAAGCCCGGCATGGACGGCCCCAAGG 2206 Qy 734 TGAAGCAGTGGCCCTGACCGAGGAAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGA 793 Db 2207 TGAAGCAGTGGCCCTGACCGAGGAAGATCAAGGCCCTCGACCGCCATCTGCGGAGGAGA 2266 Qy 794 TGGAAAAGGAGCCAAGATCACCAAGATCGGCCCTGACCCCCCTGACACCCCCCGTGT 853 Db 2267 TGGAGAAGGAGAACACCCCAAGATCGCCCCCCGGAACCCCCCGTGT 2326 Qy 854 TGGCCATCAAGAAGACACCCCAAGTCGCCCCAAGACCCCCCGTGT 2326 Qy 854 TGGCCATCAAGAAGACACCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGA 2186 Qy 854 TGGCCATCAAGAAGACACCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGA 2186 Qy 854 TGGCCATCAAGAAGACACCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGA 2186 Qy 914 ACAAGCGCACCCAGGACTTCTGGGACCTGGCGCAAGCTGGTGGACTTCCGCCGCGGCTGA 2186 Qy 914 ACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGTGGCCCCCCCC	974 AGAAGAAGAGCGTGACCGTGACGTCGGCGTACTTCAGCGTGCCCTGG [0y 1154 AGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGGCACCCCGAGATCGTGATCT 1213 1	Qy 1334 AGGACCCCCTTCCTGGATGGGTACGAGCTGCCCCGACAAGTGGACCGTGCAGC 1393 bb 2807 AGGACCCCCTTCCTGCCCATCGAGCTGCACCCGACAAGTGGACCGTGCAGC 2860 Qy 1394 CCATCGAGCTGCCCGAGAAGGAGAGTGGACCGTGAACGACATCCAGAAGCTGGTGCGCA 1453 Db 2861 CCATCGAGCTGCCCGAGAAGGAGACTGGACCGTGAACGACATCCAGAAGCTGGTGGGCA 2920 Qy 1454 AGCTGAACTGGGCCAGAATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGC 1513 Db 2921 AGCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGC 2980
Qy 2234 AGCAGCTGATCAAGAAGGAGAAGCTGACCTGAGCTGCCCGCCC	RESULT 11 US-10-190-435-10 Sequence 10, Application US/10190435 Fublication No. US20030143248A1 GENERAL INFORMATION: APPLICANT: BARNETT, Susan APPLICANT: APPLICANT: ASSISTANT ON TYPE CONTRENT ON TYPE PROBABLICANT ATTLE OF INVENTION: POLYMEDIDES, POLYPEPTIDES AND USES THEREOF TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/190,435 CURRENT PILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 319 SOFTWARE: PALENTIN Ver. 2.0 SEQ ID NO 10 LEMCTH: 3930 TYPE: DNA	S-1 Ou Be Ma Ma	AGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGCCACATCGCCCGCAAGGGCCCCAAGCGCCACATCGCCCGCAAGGGCCCCCAAGCGCATCATCAACTGCGGCAAGGAGGGCCACATCGCCGCAACGCCCCCAAGCGCCACATCGCCGCAACGCCCCCCCC	254 AGGCCGCGGAGTTCCCCAGGGGGGGAGCCGACCCCCCCCC

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TYPE: DNA
ORGANISM: Artificial Sequence
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          TGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGC
                                                 AGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCCACCACCACAACCA
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TGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGC
                                       TGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCA
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RESULT 12
US-10-190-435-11
US-10-190-435-11
Sequence 11, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
HAPPLICANT: BARNETT, SUSAN W.

1606 1666 1726 1786 1846 1906 1966 2026 2086 2146 2206 613 2207 TGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCATCTGCGAGGAGA 2266 133 193 ; OTHER INFORMATION: Description of Artificial Sequence: GagComplPolmutIna_C US-10-190-435-11 253 313 493 553 673 733 373 433 793 667 AGGACTGCACCGCGAGCCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCA AGGCCCCCAAGCCCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCCGCA 134 ACTGCCGCCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA ACTGCCGCGCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGAAGGGCCACCAGATGA AGGACTGCACCGAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCA 1727 AGSCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGC AGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGGAGCGCCCAGGGCACCTCGAACT 1847 TCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 434 AGGAGGCCCTGCTGGACACCGGCGCCGACGACACGTGCTGGAGGAGATGAGCCTGCCCG GCAAGTGGAAGCCCCAAGATGATCGCCGCCATCGGCGCTTCATCAAGGTGCGCCAGTACG 1967 GCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACG 554 ACCAGATCCTGATCGAGATCTGCGCCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCA 2027 ACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGATCGGCCCA CCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGCCCCAAGG 2147 ccarcagececarcagacegraecergaageraaacraaagecegaargaacegececeaaage TGAAGCAGTGGCCCTGACCGAGGAGAGATCAAGGCCCTGACCGCCATCTGCGAGGAGA 14 TGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTCA TCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 614 CCCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCTGCACCTTGC υ APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: ENGELBRECHT, Susan
APPLICANT: ENGELBRECHT, SETTELLICA J.
TITLE OF INVENTION: POLYNETIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT APPLICATION NUMBER: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 11
LENGTH: 3930 9 Length 3930; Indels 15; 5 DB Query Match 98.0%; Score 2414; L Best Local Similarity 99.5%; Pred. No. 0; Matches 2433; Conservative 0; Mismatches 674 734 ò 셤 ð 엄

1914 CCGACTACTGGCAGCCACCTGATCCCCGAGTGGGAGTTCGTGAACCCCCCCC	RESULT 13 US-10-190-435-58 Sequence 58, Application US/10190435 Sequence 58, Application US/10190435 Sequence 58, Application No. US20030143248A1 GENERAL INFORMATION: GENERAL INFORMATION: THIS APPLICANT: ENGELBECHT, Susan TITLE OF INVENTION: POLYBECTHISS, POLYBETHIDES AND USES THEREOF TITLE OF INVENTION: POLYBETHIDES, ENCODING ANTIGENIC HIV TYPE C TITLE OF INVENTION: POLYBETHIDES, POLYBETHIDES AND USES THEREOF TITLE OF INVENTION: POLYBETHIDES, POLYBETHIDES AND USES THEREOF TITLE OF INVENTION: DATE: 2002-18133 CURRENT FALLING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 319 SOFTWARE: PATENTION OF: 2.0 SEQ ID NO 58 SEQ ID NO 59 SEQ ID NOS: 319 SEQ ID NO 59 SEQ ID NOS: 319 S
TGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGGGAACCCCTACAACACCCCCGTTT 194 TGGAGAAGGAGGGAACACCCCAGGAACCCCCGTTT 126	1394 CCATCGAGCTGCCCGAAAGGAGGCTGGACCGTGAACGACTCCAGAAGCTGGTGGGCA 1453

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                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: GagPolmut_C
                                                                                                                                                                                                                                           DB 15; Length 3531;
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REPERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                        Score 2383.6;
Pred. No. 0;
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Best Local Similarity 98.8%;
Matches 2414; Conservative (
                                                                                                                                                TYPE: DNA
ORGANISM: Artificial
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Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: WORLERECHT, Susan
APPLICANT: WORLERECHT, Susan
APPLICANT: VAN RENSBURG, Estrelita J.
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  CTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCTGC
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source 12469 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="PR975(+)"	Query Match 98.3%; Score 2415.4; DB 6; Length 2469; Best Local Similarity 99.3%; Pred. No. 3.2e-243; Matches 2451; Conservative 0; Mismatches 6; Indels 12; Gaps 2;	QY 1 GTCGACCACCATGGCCGAGGCCATGAGCCACCAGCGCCAACATCCTGATGCAG 60	Qy 61 CGCAGCAACTICAAGGGCCCCAAGGGATCATCAAGTGCTTCAACTGCGCAAGGGGC 120	Qy 121 CACATCGCCCGCAACGACCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGGG 180 Db 121 CACATCGCCCGCGAACTGCCGCGCCCCCCGCAAGAGGGCTGCTGGAAGGGCTGCGGCAAGGAG 180	Qy 181 GGCCACCAGATGAAGGACTGCACCAGGCCCAGGCCCAACTTCTTCCGCGAGGACCTGGCC 240	Oy 241 TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGGCCAACAGCCCCACC 300	QY 301 AGCGGGGGGTGCGGGGGGGGACAACCCCGCAGGGGGGGGG	Qy 361 GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCTCAAGGTG 420 bb 361 GGCACCCTGAACTTCCCCCCAGATCACCCTGTGGCAGCGCCCCTTGGTGAGCATCAAGGTG 420	Qy 421 GGCGGCGAGATCAAGGAGCCCTGCTGGACACCGCCGACGACGACGACGACGAGGAG 480 bb 421 GGCGGCCAGATCAAGGAGCCCTGCTGGAGCACCGACGACGACGACGACGACGACGACGAGAGGAG	QY 481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAG 540 Db 481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAG 540	Oy 541 GTGCGCCAGTACGACTCGGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG 600	QY 601 CTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGCTG	661 ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGAAGCTGAAGCCGGCATG	Db 721 GACGCCCCAAGGTGAACAGTGGCCCTTGACCGAGGAAAAAATCAAGGCCCTGACCGCC 780	Qy 781 ATCTGCGAGGAGATGGACAAGATGGGCAAGATCGGCCCCGAGAACCCCTAC 840 Db 781 ATCTGCGAGGAGTGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 840	Qy 841 AACACCCCGTGTTCGCCATCAAGAAGAAGAAGAAGACACCAAGTGGCGCAAGTGGCGCAAGTGGCGCAAGTGGCGCAAGTGGCGCAAGTGGCGCAAGTGGCACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGCACCAAGTGGCGCAAGTGGCGCAAGTGGCCCAAGTGGCACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAACAAC	901
	Qy 1795 AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG 1854	Qy 1855 GAGACCTGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1914 Db 1861 GAGACCTGGTGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1920	Qy 1915 ACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGCCCATCATCGGCGGAG 1974	Qy 1975 ACCTTCTACGTGGACGCCGCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG 2034	OY 2035 ACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCCAACCGAAGACCGAG 2094	QY 2095 CTGCAGGCCATCCAGCTGGACCAGCGGCGAGGGGAGGTGAACATCGTGACCGAC 2154 Db 2101 CTGCAGGCCATCCAGCTGGACCAGCGACGAGCGAGGTGAACATCGTGACCGAC 2160	Qy 2155 AGCCAGTACGCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGGCGAGCTGGTG 2214	Qy 2215 AACCAGATCATCGAGCAGCTGATCAAGAAGAGAAGGGTGTACCTGAGCTGGGTGCCCGCC 2274	Qy 2275 CACAAGGGCATCGGCGGCAACGAGGAGAAGCTGGTGAGCAAGGGCATCCGCAAG 2334 	Qy 2335 GTGCTGTTCCTGGACGCCATCGACGCGCATCGTGATCTACCAGTACATGGACGACCTG 2394	Qy 2395 TACGTGGGCAGCCGCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACGTGAA 2454 	Qy 2455 TTC 2457 	AX455914 2469 bp	DEFINITION Sequence 30 from Patent WO0204493. ACCESSION AX455914 VERSION AX455914.1 GI:21714899	ACTIONS SYNTHETIC CONSTRUCT ORGANISM SYNTHETIC CONSTRUCT OTHER SEQUENCES; artificial sequences.	KEFEKENUE 1 AUTHORS zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. TITLE Polynucleotides encoding antigenic hiv type c polypeptides, polyneptides and uses thereof	JOURNAL Patent: WO 0204493-A 30 17-JAN-2002; CHIRON CORPORATION (US) ; University of Stellenbosch (ZA) FEATURES Location/Qualifiers

QY 2029 TACGTGACCGGCGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAACCA	2209	CCCGCCCACAGGGCCATCGGCGCAACGGCGCAACGGCAAGGCCACACGCCCCACAGGCCACGCCACAGGCCACGCCCCCACAGGCCACGCCGC	Qy 2389 GACCTGTA.GGGGGGCGGGCCCTAGGATTAAAAGCTTCCCGGGGGTAGGACC 2448 Db 2401 GACCTGTA.GGTGGGCGGCGCCTAGGATTAAAAGCTTCCCGGGGCTAGCACC 2460 Qy 2449 GGTGAATTC 2457 Db 2461 GGTGAATTC 2469	z	~	REFERENCE 1 (bases 1 to 2300) AUTHORS Barnett,S., Megede,J.Z., Srivastava,I., Lian,Y., Hartog,K., Liu,H., Greer,C., Selby,M. and Walker,C. TITLE Improved expression of HIV polypeptides and production of virus-like particles	JOURNAL Patent: JP 2002533124-A 72 08-OCT-2002; CHIRON CORP COMMENT OS Artificial Sequence PN JP 2002533124-A/72 PD 08-OCT-2002	PF 30-DEC-1999 UP 2000591193 PR 31-DEC-1998 US 60/114495,01-DEC-1999 US 60/168471 PI SUSAN BARRETT, JAN ZUR MEGEDE, INDRESH SRIVASTAVA, YING LIAN, PI KARIN HARTOG PI HONG LIU, CATHERINE GREER, MARK SELBY, CHRISTOPHER WALKER PC C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P31/18, A61P37/02, PC	2N5/10, C12N Scripti	FI SOULCE I. 2500 FT Location/Qualifiers FEATURES Location/Qualifiers 1. 2300	/organism="gynthelic construct" /mol_type="gynthelic DNA" /db_xref="taxon:32630"
DD 901 TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGAGGTGCAGCTGGGCATCCCCCAC 960	1081 AACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCCA	Oy 1201 GAGATCCTGATCTACCAGGCCCCCTGTACGAGCGACCTGGAGATCGGC 1254 Db	Qy 1315 CCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCATCGAGCTGCACCCC 1368 Db	Oy 1429 ATCCAGAAGCTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG 1488 Db		1609 GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAG 	QY 1669 TGGACCTACCAGATCTACCAGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1728 D	1741 ATGGGCACCGCCACCACGACGACGAGAGCTGACCGAGGCCGTGCAGAGAGCCCCCACCAACGAAGAATCGCCCAACGAAGAACCCCCAACGAAGAACCCCCAACGTTCCGCCTGCCCATCCAGAAGAAGCAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	Oy 1849 ACCTGGGAGCTGGACCGACTACTGGCAGCCACCTGGATCCCGAGTGGGAGTTC 1908 Db 1861 ACCTGGGAGACTGGACGACTACTGGCAGCCACCTGGATCCCCGAGTGGGAGTTC 1920	OY 1909 GTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAGGAGCCCATCATCGGC 1968	OY 1969 GCCGAGACCTTCTACGTGGACGCCGCCGACCGCGACCGAGACCGAGGCCGCGC 2028

1178 ACCCCTTCCCCCACACCCCCCACATCCCTCACACCCCCCC	1981 TGAACATCGTGACCGTCAGCCCTGGGCATCATCAGCTCTGGCCCAGCCCAGAAA 2040 2198 GCGAGAGCCGCTGAACCAGTCATCACCAGCCTGAGCATCAGAGAAGAAGAAGAACGTGATCC 2257 2041 GCGAGAGCCAGCTGATCATCGAGCAGCTGATCAAGAAGAAGAAGAAGATGACC 2100 2258 TGAGCTGGTGACCACAAGGCCATCGGCGGCAACGAGAGAAGAAGGTGAACC 2100
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Initiarity 93.64; Score 2040; DB 6; Length 2300; Conservative 0; Feel Not. 46.244 155; Indels 12; Gaps GCGGCAAGGGGAAGCCCCCCCCCCCCCCCCCCCCCCC	1058 CTTCACCACCAGCAGCATCAACAACGCGGCACCCGGCTACCAGTACAACGGCT 1117 901 CCTTCACCATCCCCAGCATCAACAAGACCCCCGGCATCCGCTACCAGTACAACGGCT 1117 1118 TGCCCCAGGGCTGGAAGGGCGCCCCAGCATCTTCCCAGAGCACCAGAGACCCAGGTACCAGG 1177 1118 TGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGG 1177 961 TGCCCCAGGGCTGGAAGGCCCCCCCCCCCACATCTTCCAGAGCAGCATGACCAAGATCCTGG 1020

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ive 0; Mismatches 135; Indels 12
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	RESULT 7 BD263704 LOCUS BD263704 LOCUS DEFINITION Improved expression of HIV polypeptides and production of virus-like particles. ACCESSION BD263704. IG:33073472 KEYWORDS JP 2002533124-A/71. SOURCE ORGANISM Synthetic construct ORGANISM ORGANISM ORGANISM ORGANISM ORGANISM ORGAN	AL Patricles Artificial Sequence OS Artificial Sequence OS Artificial Sequence OS Artificial Sequence PN 4D 2002533124-A/71 PD 08-OZT-2002 PF 30-DEC-1999 JP 2000591193 PR 31-DEC-1999 US MEGEDE, INDRESH SRIVASTAVA, YING LJ KARIN HARTOG, PJ HONG LJU, CATHERIUR GREER, MARK SELBY, CHRISTOPHER WA CCI2NIS, O9, AGIK31/711, AGIK38/00, AGIR48/00, AGIP31/18, AGIR CL2NIS/10, PC PC CL2NIS/10, PC P	FT source 12306 FRATURES Location/Qualifiers 12306 Source 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12306 12	Query Match 82.2%; Score 2019.2; DB 6; Length 2306; Best Local Similarity 93.2%; Pred. No. 6.8e-202; Matches 2150; Conservative 0; Mismatches 138; Indels 18; Gaps 3; Qy 170 GGGGAAGGAGGACCACAGATGAAGGACTGCACGAGGCCAAGTTCTTCCGCG 229 Db 1 GCGGCGGAAGGACCAAATGAAAGAATGAAAGAACAGAGAACAGAACTTCTTCCGCG 60 Qy 230 AGGACTTGCCTGCAAGGAAGGCCCGCGAGTTCCCAGCGAGTAATTTCTTCTCGCG 60 Db 61 AGGACCTGGCCTTCCTGCAGGCAAGGCCCGCGAGTTCCAGCGAACAGACAG
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Liu, H., Greer, C., Selby, M. and Walker, C.
Improved expression of HIV polypeptides and production of
virus-like particles
Patent: EP 1431851-A 82 30-JUN-2004;
CHIRON CORPORATION (US)
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/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence:
FS(-).protmod.RTopt.YM"
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                                              TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCG
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PI HONG LIU, CATHERINE GREER, MARK SELBY, CHRISTOPHER WALKER PC
CI2N15/09,A61K31/711,A61K38/00,A61K48/00,A61P31/18,A61P37/02,
CI2N5/10,
PC C12N7/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: FS(-).protmod.RTopt(+) FH
Location/Qualifiers
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Pred. No. 1e-199;
0; Mismatches 141; Indels
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/organism='Artificial
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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1861 AGACCAAGCTGGGCAACGCTACCGTCACCGGCGGCAGAAGGTGGTGACA 1920 2066 TGACCGAGCCACCAACCAGAAGACCGAGCTGCAGGCCTCGCGGCGCAGAACA 125	2221 TCGTGATCTACAGATCAGACCTGTACGTGGGCGGCCCTAGG 2426 AAAAGCTTCCCGGGGCTAGCACCTGTAATTC 2457 [11	TITLE Improved expression of HIV polypeptides and production of virus-like particles JOURNAL Patent: EP 143851-8 #4 30-JUN-2004; FEATURES CHIRON CORPORATION (US) FOATURES 12312 /mol type="unassigned DNA" //mol type="unas	Query Match 81.3%; Score 1998.4; DB 6; Length 2312; Best Local Similarity 92.9%; Pred. No. 1e-199; Matches 2147; Conservative 0; Mismatches 141; Indels 24; Gaps 4; Qy 170 GGGGCAAGAGGGCCACCAGATGAAGGATGCACGAGCCCAGGCCAACTTCTCGGG 229 Db 1 GGGGCGGAAGACACCAAATGAAAGATTGCACGAGAGAGACAGAC

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Barnett, S.W., Megede, J., Greer, C. and Selby, M.

Expression of HIV polypeptides and production of virus-like
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Patent: US 6602705-A 84 05-AUG-2003;
Location/Qualifiers
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/mol_type="genomic DNA"
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1790 TGGAGAGCATCGTGATCTGGGGCAAGACCCCAAGTTCCGCCTGCCCATCCAGAAGGAGA 1849
                                                               4763 CCGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCAAGCTGCCCATCCAGAAGGAGA 4822
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May 31, 2005, 23:20:00; Search time 1264.25 Seconds (without alignments) 11504.726 Million cell updates/sec

US-09-610-313B-32 2457

Title: Perfect score:

1 gtcgacgccaccatggccga.......ggggctagcaccggtgaattc 2457 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

N_Geneseq_16Dec04: Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abl39961 Synthetic	Adm73766 HIV-1 pol	Aca03546 Synthetic	Adc13264 DNA of HI	Adc13230 DNA of HI	Abl39960 Synthetic	Adm73765 HIV-1 pol	Adc13231 DNA of HI	Adc13232 DNA of HI	Aca03591 Synthetic	Adc13279 DNA of HI	Aca03547 Synthetic	Adc13265 DNA of HI	Abl39959 Synthetic	Adm73764 HIV-1 pol	Adc13234 DNA of HI	Aca03548 Synthetic	Adc13266 DNA of HI	Adc13236 DNA of HI	Aca03521 Synthetic	
SUMMARIES	ID	ABL39961	ADM73766	ACA03546	ADC13264	ADC13230	ABL39960	ADM73765	ADC13231	ADC13232	ACA03591	ADC13279	ACA03547	ADC13265	ABL39959	ADM73764	ADC13234	ACA03548	ADC13266	ADC13236	ACA03521	
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	Score	2457	2457	2443.4	2443.4	2436.4	2436.2	2436.2	2434.8	2434.8	2434.8	2434.8	2428.6	2428.6	2415.4	2415.4	2404.4	2403.4	2403.4	2402.8	2401.8	
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Adc13233 DNA of HI	Adc13235 DNA of HI	Aca03551 Synthetic	Adc13269 DNA of HI	Aca03549 Synthetic	Adc13267 DNA of HI	Aca03550 Synthetic	Adc13268 DNA of HI	Aca03541 Synthetic	Acc78505 HIV p2Pol	Acc78488 HIV GagPo	Acc78489 HIV GagPo	Aca03522 Synthetic	Adc13238 DNA of HI	Acc78484 HIV GagCo	Acc78485 HIV GagCo	Acc78486 HIV GagCo	Aca03584 Synthetic	Acc78529 HIV TatRe	Aca03592 Synthetic	Adc13280 DNA of HI	Adc13237 DNA of HI	Aca03542 Synthetic	Acc78506 HIV p2Pol	Aca03545 Synthetic
ADC13233	ADC13235	ACA03551	ADC13269	ACA03549	ADC13267	ACA03550	ADC13268	ACA03541	ACC78505	ACC78488	ACC78489	ACA03522	ADC13238	ACC78484	ACC78485	ACC78486	ACA03584	ACC78529	ACA03592	ADC13280	ADC13237	ACA03542	ACC78506	ACA03545
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ALIGNMENTS

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds. Synthetic construct PR975YMWM SEQ ID NO:32 Human immunodeficiency virus; type C. ABL39961 standard; DNA; 2457 BP. 05-JUL-2001; 2001WO-US021241. 05-JUL-2000; 2000US-00610313. (first entry) WO200204493-A2. 15-MAY-2002 17-JAN-2002. Synthetic ABL39961; ABL3996.

(CHIR) CHIRON CORP. (UYST-) UNIV STELLENBOSCH.

Barnett SW, Zur Megede J,

Engelbrecht S, Van Rensburg EJ;

WPI; 2002-154920/20.

New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.

Claim 1; Fig 10; 233pp; English.

The present invention describes expression cassettes comprising a polymucleotide sequence encoding a polymetide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gay, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy.

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The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGCATG
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                                                                    Query Match 100.0%; Score 2457; DB 6; Length 2457; Best Local Similarity 100.0%; Pred. No. 9.7e-296; Matches 2457; Conservative 0; Mismatches 0; Indels 0;
                                                       G; 300 T; 0 U; 0 Other;
                                                       A; 837 C; 754
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also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polymucleoride sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polymucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2457; DB 12; Length 2457; 100.0%; Pred. No. 9.7e-296;
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                                                                                                                                                                                                                                                                                                                                                             Sequence 2457 BP; 566 A; 837 C; 754 G; 300 T; 0 U; 0 Other;
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Matches 2457; Conservative
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The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                       Example 1; Fig 34; 262pp; English.
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Query Match 99.4%; Score 2443.4; DB 8; Length 2445; Best Local Similarity 100.0%; Pred. No. 4.7e-294; Matches 2444; Conservative 0; Mismatches 1; Indels 0; Gaps		GCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGC	67 AACTTCAAGGGCCCCAAGGGATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATC 126 67 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCCCGCAACTGCCGCCCCCCCCAAGAAGAGCTGCTGGAAGTGCGGCAAGGAGGCCAC		187 CAGATGAAGGACTGCACCGAGGCGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCC 246	181 CAGATGAAGGACTGCACCGAGGGCCAGGCCAACTTCTTCCGCGAGGACTTGCTCGC 240	247 CAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAAACCGCGCCAACAGCCCCACCAGCCGC 306	241 CAGGCCAGCCCGCGGAGTTCCCCAGCGGGCGGGCCCACCAGCCCCCACCAGCCGC 300	307 GAGCTGCAGGTGCGCGGCGACCCCCGCAGCGAGCCGGCGCGAGGCGCCAGGGCACC 366	301 GAGCTGCAGGTGCGCGGCGACAACCCCCGCAGGCCGGCGCGGCGCGCGGGGCCAGGGCACCCAGGGCACCCAGGGCAGGCCAGGGCAGGCCAGGGCAGGCAGGCCAGGGCAGGCCAGGGCAGGGCAGGCCAGGGCAGGCAGGCAGGCCAGGGCAGGCAGGCCAGGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGCAGGAGAGAAGA	367 CTGAACTTCCCCCAGATCACCCTGTGGCAGGCCCCCTGGTGAGCATCAAGGTGGGCGGC 42/	361 CTGAACTICCCCCAGATCACCCTGTGGCCCCCCTGGTGAGCATCAAGGTGGCGCC 420	427 CAGATCAAGGAGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGC 486	421 CAGATCAAGGAGGCCCTGCTGCCCACCGGCGCCGACGACGACGACGAGGAGGAGATGAGC 480	487 CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGC 54	481 CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGC 540	547 CAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAGGCCATCGGCACCGTGCTGATC 606	541 CAGTACGACCAGATCCTGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATC 600	607 GGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTG 666	601 GGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTGGGCTGCACCCTG 660	667 AACTICCCGATCAGCCCCATGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGC 726	661 AACTICCCCATCAGCCCCATGAGCCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGC 720	727 CCCAAGGTGAAGCAGTGGCCCCTGACGAGGAGAAGATCAAGGCCCTGACCGCCATCTGC 786
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<u>ک</u> ک	967	GGCCTGAAGAAGAAGAGGCGTGACCGTGGACGTGGGGCGACGCCTACTTCAGCGTG 1026
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දු දු	1087	ACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCACCCCAGC 1146
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è	1207	GTGATCTACCAGGCCCCCCTGTACGTGGGAGCAGCGACCTGGAGATCGGCCAGCGCGCC 1266
qq	1201	GTGATCTACCAGGCCCCCCTGTAGGTGGGCAGCGAGCTGGAGATCGGCCAGCACGCGGCC 1260
è d	1267	AAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGCTGGGGCTTCACCACCCCCGACAAGAAG 1326
ò	1327	CACCAGAAGGAGCCCCCTTCCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAG 1386
QQ	1321	CACCAGAAGGAGCCCCCTTCCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAG 1380
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දු පු	1447	AAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAGGTGCGCCACTGTGCAAGGTG 1506
à	1507	CTGCGCGGCGCCAAGGCCCTGACCGACGTCGTGCCCTGACCGAGGAGGCCGAGGTGGAG 1566
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<u>ک</u> ۾	1567 1561	CTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGC 1626
ò	1627	AAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTAC 1686
qa	1621	AAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTAC 1680
ò	1687	CAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACACC 1746
. qa	1681	CAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACACC 1740
à	1747	AACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATC 1806
qq	1741	AACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATC 1800
ò	1807	TGGGGCAÀGACCCCCAAGTTCCGCCTGCCCATCCAGAAGAGAGACCTGGGAGACCTGGTGG 1866

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encoding

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The invention relates to a novel expression cassette comprising a polymucleotide sequence encoding a polypeptide including an HIV Gag. Int, Nef, plSmaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, intradermally, transdermally, intravaginally, intravectully, orally or intravenously. The expression cassette is useful polymentation, generating packaging cell lines and producing HIV polymelecide sequence represents the DNA of an HIV Type C related sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTTCAAGGGCCCCAAGGGCATCATCAAGTGCTTCAACTGCGGGAAGGGGGCCACATC 126
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                        New expression cassette comprising a polynucleotide sequence enco
polypeptide including an HIV Gag, Env. Int. Nef. pisRnaseH, Pol.,
Prot. or Rev polypeptide, useful for immunization, or generating
packaging cell lines.
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                                                                                              Disclosure, Fig 40; 301pp; English.
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Matches 2444; Conservative
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Rev; HIV type C; gene therapy;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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Qy 1807 TGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGAACCTGGGAAACCTGGTGG 1866 Db 1801 TGGGGCAAGACCCCCAAGTTCCGCCTGCCAAGAGAAGACCTGGAAGAACCTGGAAGACCTGGAAGACCTGGAAGACCTGGAAGACCTGGAAGACCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCCCCCCC		2161 CTGGGCATCATCAAGAAGAGAAGCGAGCGAGCGAGCTGGTGAACCAGATCATC 2227 GAGCAGCTGATCAAGAAGGAGAAGCGAGCGAGCTGGTGAACCAGATCATC 2221 GAGCAGCTGATCAAGAAGGAGAAGCTGATACCTGAGCTGGTGCCCGCCC	Oy 2407 GGGGCCCTAGGATTAAAAGCTTCCCGGGGCTAGCACCGGT 2451	DIA OF HIV construct GagComplPolmut_C SEQ ID NO 9. XX XX XX XX XX XX XX XX Expression cassette; HIV Gag; Env; Int; Nef; pl5RnaseH; Pol; Tat; Prot; XX XX XX XX Human immunodeficiency virus. XX
AACTTCCCCATCAGCCCCATCGAGCCCGTGAAGCTGAAGCTCGACATGGACGC 720 CCCAAGGTGAAGCAGTGGCCCTGACCGAGAGAAGATCAAGGCCCTGACCGCCATCTGC 786 [907 GAGCTGAACAAGCGCACCAGGAGGTGCAGCTACGCCATCCCCCACCGGCC 966 901 [1087 ACCCCGGCATCCGCTACCAGTACAACGTGCTGGGGCTGGAAGGGCAGCCCCAGC	CACCAGAAGGACCCCCCTTCCTGCCCATCGAGCTGCCCGACAAGTGGACCGTGCAG	1507 CTGGGGGGGCCAAGGCCCTGACCGACCGAGGGGGGGGGG

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      WPI; 2003-221593/21
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ø encoding Pol, Tat, wew expression cassette comprising a polynucleotide sequence encopolypeptide including an HIV Gag, Env. Int. Nef. p15RnaseH, Pol. Prot. or Rev polypeptide, useful for immunization, or generating packaging cell lines.

Disclosure; Fig 6; 301pp; English

The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Ent, Nef, pismaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intransally, intransally, intransally, intraversion cassette is useful intrarectally, orally or intravenously. The expression cassette is useful polympoptides. This polymucleotide sequence represents the DNA of an HIV Type C related sequence of the invention. useful

Sequence 3930 BP; 890 A; 1365 C; 1214 G; 461 T; 0 U; 0 Other;

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1546 1966 2146 1666 1786 1846 1906 2026 2086 ö 1606 1726 133 193 253 313 373 433 493 553 613 673 73 1487 TCGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCGAGCAACTTCA ACTGCCGCGCCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA AGGACTGCACCGAGGCCAAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCA AGGTGCGCGCGCACAACCCCCGCAGCAAGCCGGCGCCCGAGGCCAGGGCACCTGAACT GCAAGTGGBAAGCCCAAGATGATCGGCGGCGCATCGGCGGCGCTTCATCAAGGTGCGCCAGTACG ACCAGATCCTGATCGAGATCTGCGGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCA CCCCCGTGAACATCATCGGCCGCAACATGCTGACCCCGGGGCTGGGGCTGCACCTTGA TGGCCGAGGCCATGAGCCAGGCCACCAGCCCAACATCCTGATGCAGCGCAGCAACTTCA AGGGCCCCAAGCGCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCA ACTGCCGCGCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGA AGGACTGCACCGAGCGCCAGGCCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCCAGGGCA AGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCCCAACAGCCCCCAGCCGCGAGCTGC **AGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGC AGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGCCGAGGCGCCAGGGCACCTGAACT** TCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA AGGAGGCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCG Agga Gecerracine a consequencia de consequencia GCAAGTGGAAGCCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACG ACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCCA CCCCCGTGAACATCATCGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCC Gaps DB 10; Length 3930; ö Indels Query Match 99.2%; Score 2436.4; DB 10, Best Local Similarity 100.0%; Pred. No. 3.2e-293; Matches 2437; Conservative 0; Mismatches 1; 1547 1607 1667 1727 1787 1907 14 74 134 194 254 314 374 1847 434 494 1961 554 2027 614 2087

à i	674	674 CCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGCCCCCAAGG 733
an (2147	CCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGGACACATGGACCCCCAAGG Z206
දු දු	734	TGAACCAGTGGCCCTGACCGAGGAGAAATTCAAGGCCCTGACCGCCATCTGCGAGGAGA 793
à	794	TEGAGAAGAAGACCCCCGAAGATCACCAAGATCGCCCCGAAAACCCCCCTGT 853
qa	2267	TGGAGAGAGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGT 2326
ò	854	TCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGA 913
QQ	2327	TCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGTGCTTCCGCGAGCTGA 2386
<u>۸</u>	914	ACAAGCGCACCAGGACTICTGGGAGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGA 973
qq	2387	
ò	974	AGAAGAAGAAGAGCGTGACCGTGGTGGACGTGGGGGACGCCTACTTCAGCGTGCCCTGG 1033
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٥٨	1034	ACGAGGACTICCGCAAGIACACCGCCTICACCATCCCCAGCATCAACAACGAGACCCCCG 1093
QQ	2507	Acgadgactrccgcaagracaccccrcaccarccccagcarcaacaacgacccccg 2566
٥y	1094	GCAICCGCIACCAGIACAACGIGCIGCCCCAGGGCIGGAAGGCCAGCCCCAGCAICTICC 1153
ΩP	2567	
δ	1154	
οp	2627	
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QQ	2687	ACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAGCGCCCAAGATCG 2746
ò	1274	
QQ	2747	
ζ	1334	
qq	2807	
ģ	1394	AGCTGCCCGAGAAGAAGAGCTGGACGTGAACGACATCCAGAAGCTGGTGGCACAGCTGA 1453
qa	2867	
λŏ	1454	ACTEGGCCAGACCAGATCTACCCGGCATCAAGGTGGGCCAGCTGTGCAAGCTGCTGCGGG 1513
QQ	2927	
δ	1514	GCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCG 1573
οg	2987	
λ	1574	AGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACC 1633
qa	3047	310
δ	1634	16
qq	3107	31
δ		17
QQ	3167	m

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type C; antigenic HIV type C protein;
immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef;
immunostimulant; gene therapy; gene; ds.
TGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGGCATCGTGATCTGGGGCA
           TGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTCGGGGCCA
                                                                                              TGTGGTACCAGCTGGAGAAGAAGCCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCG
                                                                                                         AGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACT
                                             AGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGCCTGGGAGACCTGGTGGACCGACT
                                                                                                                              AGATCGTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                CTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT 2451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic construct PR975YM SEQ ID NO:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus; type
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                                                                                                                                                                                                                                                                                                                                                                                                                        ABL39960 standard; DNA; 2463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymucleotide sequence encoding a polymetria comprising a polymucleotide sequence encoding a polymetria comprising a type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polymucleotides are useful in applications including DNA immunisation of packaging cell lines, and production of HIV Type C proteins. The polymucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06205 represent sequences used in the exemplification of
                                                                                                                                                                                                                                 Type C polypeptides, useful : generation of packaging cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes expression cassettes comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.2%; Score 2436.2; DB 6; Length 2463; Best Local Similarity 99.6%; Pred. No. 3.6e-293; Matches 2454; Conservative 0; Mismatches 3; Indels 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2463 BP; 567 A; 835 C; 759 G; 302 T; 0 U; 0 Other;
                                                                                                  Van Rensburg
                                                                                                                                                                                                                              New polynucleotides encoding antigenic HIV applications including DNA immunization or lines, particularly in gene therapy.
                                                                                                  ŝ
                                                                                                  Engelbrecht
                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 9; 233pp; English.
                                                                                               Zur Megede J, Barnett SW,
CHIRON CORP.
UNIV STELLENBOSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention
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The invention relates to an expression cassette comprising a polymucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polymucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polymucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polymucleotide of the invention.
                                                                                                                                                                                                                                                                         New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
                                                                                                                                                                                                   Rensburg EJV;
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                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 31; 160pp; English
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                  05-JUL-2001; 2001US-00899575
                                                       05-JUL-2000; 2000US-00610313
                                                                                              MEGEDE J Z.
BARNETT S W.
ENGELBRECHT S.
RENSBURG E J V.
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                                                                                                                 (BARN/) (ENGE/) (RENS/)
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Sequence 2463 BP; 567 A; 835 C; 759 G; 302 T; 0 U; 0 Other;

240 420 120 CGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCGCAAGGAGGGC 120 180 240 300 360 420 480 480 TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCCAGCGAGCAGAACCGCGCCAACAGCCCCAACA 9 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCCCCCCTGGTGAGCATCAAGGTG CACATCGCCCCCCAACTGCCGCCCCCCCCCCAAGAAGGCTGCTGGAAGTGCGGCAAGGAG GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCC TTCCCCCAGGGCAAGGCCCGCGAACTTCCCCAGCGAGCAGAACCGCGCCCAACAGCCCCACC GTCGACGCCACCATGGCCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG CGCAGCAACTTCAAGGGCCCCCAAGCGCATCAAGTGCTTCAACTGCGGCAAGGAGGC GCCACCAGATGAAGGACTGCACCGAGCCCAAGCCCAACTTCTTCCGCGAGGACCTGGCC AGCCGCGAGCTGCAGGTGCGCGCGCGACAACCCCCGCAGCGAGGCCGCCGAGCGCCCAG GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCGCCCCCTGGTGAGCATCAAGGTG Gaps DB 12; Length 2463; 9 3; Indels Score 2436.2; DB 12 Pred. No. 3.6e-293; 0; Mismatches 3; ; 99.2%; Conservative Best Local Similarity Matches 2454; Conserv 61 121 241 Query Match Best Local & 61 121 181 181 241 301 301 361 361 121 421 g 8 6 g ò 8 B 8 & 8 දු ද 8 ઠે

1020 1020 1140 1140 1374 1380 1440 1494 1434 900 960 CTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG 1554 GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGCGTGTAC 1614 540 600 999 99 720 720 780 780 840 840 900 960 ATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATCGGCGGCATCGGCGGCGTTCATCATCAAG GTGCGCCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG ATCTGCGAGGAGAGAGAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC CCCGCCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGCGGGCGACGCCTACTTC AGCGTGCCCCTGGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC cedeccaacarceaceacerececaacerecrecrecrececresecrreaceaceaceaceac AAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAG TGGACCGTGCACCGATCGAGCTGCCCGAGAAGGAGAGGAGAGCTGGACCGTGAACGACCATCCAG AAGCTGGTGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG AAGCTGGTGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGGATCAAGGTGCGCCAG ATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCGGCGGCGATCGGCGGCTTCATCAAG GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGACGCCATCGGCACGTG ACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG Accerdaactroccearcagececeareaaceareareceraaaceraaaceceare GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC ATCTGCGAGGAGATGGAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC AACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGGACGTGGACGCCGACGCCTACTTC AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCCAGGGCTGGAAGGGCAGC CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC GAGATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC AAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCAT-----CGAGCTGCACCCCCGACAAG TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAG CTGTGCAAGCTGCTGCTGCGCGCGCCCAAGGCCCTGACCGACATGGTGCCCCTGACCGAAG CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCGTGGGGCTTCACCACCCCCGAC 1435 1555 481 481 541 541 601 601 661 661 721 781 781 841 841 901 1021 1021 1081 1081 1141 1141 1201 1201 1261 1261 1321 1321 1375 1381 1441 1495 1501 721 901 196 961 셤 ò 셤 ઠે 셤 셤 요 요 g 셤 셤 셤 ઠે ઠે ठ 8 6 ે Š 8 8 ઠે 요 ठ ద ò 셤 ठ ઠ 셤 ò 셤 ð ò 셤 ઠે

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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Env, Int, Nef, piSrasseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intraveginally, intravectally, orally or intravenously. The expression cassette is useful for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymolectide sequence represents the DNA of an HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 TCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCA 433
                p15RnaseH; Pol; Tat; Prot;
                                                                                                                                                                                                                                                                                                                             New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, pl5RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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                                                                                                                                                                                                                                                                          Rensburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2434.8; DB 10; Length 3930;
Pred. No. 5.1e-293;
0; Mismatches 2; Indels 0;
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                 expression cassette; HIV Gag; Env; Int; Nef; p15RnaseH; Pol
Rev; HIV type C; gene therapy; vaccine; immunisation; HIV;
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                Nef;
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                Env; Int;
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              HIV Gag;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                         immunodeficiency virus.
                                                                                                                                            05-JUL-2002; 2002WO-US021420.
                                                                                                                                                                                                                                                                          Barnett SW,
                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP. (UYST-) UNIV STELLENBOSCH.
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Matches 2436; Conservative
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GCCGAGCTGGAGCTGGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTAC
                                                                     TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC
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1787 AGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGCGCGGGCGCCAGGGCACCCTGAACT 1846
                                                       GCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACG
                                                                                                                                                                                                                                                                              2027 ACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immunosenses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
                                                                                                                      Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
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                                                                                    Synthetic DNA ecoding immunogenic HIV peptide #74.
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254 AGGCCCCGAGGTTCCCCACCAAACCCCCCCAACAGCCCCCAACAGCCCCCAACAGCTCCCAACAGCCCCCAACAGCTCCCAACAGCTCCCCAACAGCTCCCCAACAGCTCCCCAACAGCTCCCCAACAGCTCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCAACAGCTCCCCCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACCTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCCAACACTCAACACTCCAACACTCAACACTCCAACACTCAACACTCCAACACTCCAACACTCAACACTCCAACACTCAACACTCAACACTCAACACTCAACACTCAACACTCAACACTCAACACTCAACACTCAACACACACACACACACACACACACACACACACACACAC	ACGAGGCCCCCTGAACGCCCCCCAGCCAGCCAGCCAGCCCCCCCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Enr, Nef, pisRnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to trach HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscosally, intranasally, intranscouly, intranscouly, intravenously, intravenously, intravenously, intravenously, per intravenously, reassion cassette is useful for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymocleotide sequence represents the DNA of an HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 AGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGGGCCACATCGCCCGCA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ACTGCCGCGCCCCCCGCAAGAAGGCCTGCTGGAAGTGCGGCAAGGAGGCCACCAGATGA 193
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                                                                                                                                                                                                                                                                                                  Tat; Prot;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New expression cassette comprising a polynucleotide sequence encoding polypebtide including an HIV Gag, Env. Int. Nef, p15RnaseH, Pol, Tat, Proct, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 2434.8; DB 10; Length 5184; 99.9%; Pred. No. 4.9e-293; ive 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5184 BP; 1139 A; 1852 C; 1610 G; 583 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  Pol;
                                                                                                                                                                                                                                                                                             expression cassette; HIV Gag; Env; Int; Nef; pl5RnaseH; Pol
Rev; HIV type C; gene therapy; vaccine; immunisation; HIV;
                                                                                                                                                                                                                                                DNA of HIV construct TatRevNefgagCpolina_C SEQ ID NO
CTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT 5178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Engelbrecht S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C related sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 55; 301pp; English
                                                                                                            ВР
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                            ADC13279 standard; DNA; 5184
                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus.
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                                                                                                                                                                                                      (first entry)
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UNIV STELLENBOSCH
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Matches 2436; Conservative
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                                                                                                                                                                                                      18-DEC-2003
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5141
                                                                                                                                                         ADC13279
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The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cecaecaaciicaaeeeccccaaececarcaicaaeiecricaaciececeaeeeec 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG
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                        2451
                                                                        5178
                                                                                                                                                                                                                                                                                                                                                                 Synthetic DNA ecoding immunogenic HIV peptide #30.
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                        CTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT
                                                   5141 CTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT
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                                                                                                                                                                                                          BP
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; 2001US-0316860P.
; 2002US-0349728P.
; 2002US-0349793P.
; 2002US-0349871P.
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                                                                                                                                                                                                          ACA03547 standard;
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31-AUG-2001;
16-JAN-2002;
16-JAN-2002;
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AGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCCCCCGACAAGAAGCACCAGA
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                                                   AGGAGCCCCCCTTCCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCG
                                                                              AGCTGCCCGAGAAGGAGGTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGA
                                                                                                                                                                                    AGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCAAGCTGA
                                                                                                                                                                                                                                                             ACTGGGCCAGCTACTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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                                                                                                                                                                                                                                                                                                                                                                                                      expression cassette; HIV Gag; Env; Int; Nef; p15RnaseH; Pol; . Rev; HIV type C; gene therapy; vaccine; immunisation; HIV; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 2457 BP; 564 A; 835 C; 758 G; 300 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                  HIV construct p2Pol-opt-YM_C SEQ ID NO 44.
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Pred. No. 3.2e-292;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 41; 301pp; English.
                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001; 2001US-0303192P.
31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2002; 2002WO-US021420
                                                                                                                                                                                                                                                        ADC13265 standard; DNA; 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus
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Best Local Similarity 99.6%;
Matches 2447; Conservative
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                                                                                                                                                                                                                                                                                                                                (first entry)
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(UYST-) UNIV STELLENBOSCH.
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2341 GTGCTGTTCCTGGACGCATCGATGGCGCATCGTGATCTACCAGTACATGGACGACCTG 2400
       2221 AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.
                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type C; antigenic HIV type C protein;
immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef;
immunostimulant; gene therapy; gene; ds.
                                                                                       GTGCTGTTCCTGGACGGCATCGATGCCGCCATCGTGATCTACCAGTACATGGACGTG
                                                                                                                                                               TACGTGGGCGCCGCCCCTAGGATCGATTAAAAGCTTCCCGGGGGCTAGCACCGGT
                                                                                                                                               TACGTGGGCAGCGGCCCCTAGGATCGATTAAAAGCTTCCCGGGGGCTAGCACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2469 BP; 571 A; 833 C; 761 G; 304 T; 0 U; 0 Other;
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Pred. No. 1.4e-290;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus; type C.
                                                                                                                                                                                                                                               BP,
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                                                                                                                                                                                                                                              ABL39959 standard; DNA; 2469
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Best Local Similarity 99.3%;
Matches 2451; Conservative
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                                                                                                                                                                                                                                                                                                                                Synthetic construct
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                                                           GAGATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC
                                                                                                                      CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGGCTTCACCACCCCCGGC
                                                                                                                                                         AAGAAGCACCCGCCCCTTCCTGCCCAT-----CGAGCTGCACCCCGACAG
                                                                                                                                                                      TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACGACATCCAG
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1 GTCGACGCCACCATGGCCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG

1141 CCCAGCATCTTCCAGAGCAGCATGACCAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC 1200		1419 ATCCAGAAGCTGGGGCAAGCTGAACTGGGCCAGGCCAGATCTACCCCGGCATCAAGGTG 1500 1489 CGCCAGCTGTGCAAGCTGGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACC 1548	GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCCGGGCACGACCAGGTACTACCAGAAGCCCAGGACCAGGACCAGGACCAGGATCCAGAAGCCCAGGACCAGAACCTGAAGAACCTGAAGAACCGGGAAGTACCAGGAACCAGAACCTACCAGAACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACTACCAGGAGCCCTTCAAGAACCTGAAGAACCTGAAGAACCGGCAAGTACTACAACGAACG	ATCGTG ATCGTGG ACCTGG ACCTGG ACCTGG		ACCGACAGCACTACAGCATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
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GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCCAACATCCTGATGCAG CGCAGCAACTTCAAGGGCCCCAAGCGATCATCAAGTGCTTCAACTGCGCCAAGGGGG CGCAGCAACTTCAAGGGCCCCAAGCGCATCAAGTGCTTCAACTGCCGCCAAGGGGG CACATCGCCCGCAACTGCCGCCCCCGCAAGAGGGCTGCTTCAACTGCCGCAAGGGGG CACATCGCCCGCAACTGCCGCCCCCGCAAGAGGGCTGCTGCAAGTGCGGCAAGGGGG CACATCGCCCGCAACTGCCCCCCCGCAAGAAGAGGGCTGCTGGAAGTGCGGCAAGGAG CACATCGCCCGCAACTGCCGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGAAGGGCCCCCCCGCAAGAAGGACTGCTCCCGCAAGAAGGAGGCCCCCCCC	181 GGCCACCAGATGAAGGACTGCACCGAGCCCAACTTCTTCCGCGAGGACCTGGCC 240 241 TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCAGAACCGCGCCAACAGCCCCACC 300 [ACCIGANCI ICCCCANGEGGCCCCTGACCGIGCCCGIGGAGCCGCGCCGCGCCCGCCCGCCCGAGGCCCCGAGGGGGG	### ##################################	961 CCCGCCGCCTCAAAAAAAAAAAAAAAACACGCGCTCGCTGGGGGGGG

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                   2280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
CCCGCCCACAAGGGCATCGCCACCAGCAGATCGACAAGCTGGTGAGCAGATC
                                                                               GACCTGTACGTGGGCAGCGGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGGAC
                                    CCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATC
                                                                    CGCAAGGTGCTGTTCCTGGACGGCATCGATGGTGATCTACCAGTACATGGAC
                                                                                                       GACCTGTACGTGGGCGGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACC
                                                                                                                                                                                                                                                                             HIV-1; gene; ds; HIV pol; immune response; DNA immunisation;
HIV type C protein; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rensburg EJV;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Engelbrecht S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 30; 160pp; English.
                                                                                                                                                                                                       ADM73764 standard; DNA; 2469 BP.
                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                           05-JUL-2001; 2001US-00899575;
                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2000; 2000US-00610313
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                           HIV-1 polynucleotide #7.
                                                                                                                                           GGTGAATTC 2457
                                                                                                                                                            GGTGAATTC 2469
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                                                                                                                                                                                                                                                                                                                                                                                                                        RENSBURG E J V.
                                                                                                                                                                                                                                                                                                                                                                                             MEGEDE J Z.
BARNETT S W.
ENGELBRECHT S
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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.

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            0 Other;
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            C; 761 G; 304 T; 0 U;
                                   Score 2415.4; DB 17
Pred. No. 1.4e-290;
0; Mismatches 6;
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            2469 BP; 571 A; 833
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Matches 2451, Conservative
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2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

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	Description	Sequence 32,	Sequence 4		Sequence	Sequence 3	Sequence 1	Sequence 1		Sequence 8	Sequence 4	Sequence 3
SUMMARIES	ΩI	US-09-899-575-32	US-10-190-435-43	US-10-190-305A-37	US-10-190-435-9	US-09-899-575-31	US-10-190-435-10	US-10-190-435-11	US-10-190-435-58	US-10-190-305A-82	US-10-190-435-44	US-10-190-305A-38
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de	Query Match	100.0	99.4	99.4	99.2	99.2	99.1	99.1	99.1	99.1	98.8	98.8
	Score	2457	2443.4	2443.4	2436.4	2436.2	2434.8	2434.8	2434.8	2434.8	2428.6	2428.6
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27	2136	86.9	2460	16	-190-434B-3	30,	Appl
. 28	2136	86.	2460	16	US-10-190-305A-32	32,	Appl
29	2135	86.	3564	16	US-10-241-009-13	13	Appl
30	2135	86.	3564	16	US-10-241-009-14	14	Appl
31	2135	Φ	3564	16	US-10-190-434B-13	Ë	Appl
32	2135	96	3564	16	US-10-190-434B-14	7,	Appl
33	2134.4	86.	4716	15	US-10-190-435-17	1,	App1
34	2134.4	Φ,	4716	16	-10-190-305A	Ë	Appl
35	2130.6	86.	3999		-10-241-009	o,	\ppli
36	2130.6	86.	3999	16	-10-1	o,	\ppli
37	2129	86.	3999	16	-10-241-009	2	Appl
38	2129	86.	3999	16	-10-241-009-11	11,	Appl
39	2129	86.	3999	16	-10-190-434	equence 10,	Appl
40	2129	86	3999	19	-10-190-4	11,	Appl
41	2129	86.	5283	16	-10-241-009	'n	Appl
	2129	86.	5283	16	-10-190-434B-5	Ŋ	Appl
	2129	86.	5283	16	-10-190-305A-	equence 75,	Appl
44	2128.8		4713	15	-10-190-435-5	29,	Appl
	128.	86.	71	16	US-10-190-305A-83	83,	Appl
					ALIGNMENTS		
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US-09-899	99-575-	32					
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; Publi	Publication No.	Publication No. US20	0302239	61A1			
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APPT.		Barnett	Sugar	3			
APPL	APPLICANT:	Equelbrecht, Susan	scht, Si	usan			
, APPL	APPLICANT:	van Ren	sburg,	Estre	elita Janse		
, TITL	E OF IN	TITLE OF INVENTION: POLYNUCLEOTIDES	POLYNU	CLEOI	FIDES ENCODING ANTIGENIC HIV TYPE	IV TYPE C	
; TITL	E OF IN	VENTION:	POLYPEPTIDES,	EPTI	DES, POLYPEPTIDES AND USES	THEREOF	
; FILE	FILE REFERENCE:	NCE: PPO.	PP01631.102				
CURR	ENT APPL	CURRENT APPLICATION NUMBER:	NUMBER		US/09/899.575		

9 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGGCCACCAGCGCCCAACATCCTGATGCAG 60 1 GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCCACCAGCGCCCAACATCCTGATGCAG Gaps OTHER INFORMATION: Description of Artificial Sequence: PR975YMWM DB 10; Length 2457; ; 0 Indels ; 0 0; Mismatches 100.0%; Score 2457; 100.0%; Pred. No. 0; CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver: 2.0
LENGTH: 2457 TYPE: DNA ORGANISM: Artificial Sequence Conservative Similarity Query Match Best Local Simil Matches 2457; (US-09-899-575-32 FEATURE: g ð

8 6 8 6 8 8	6
Db 2221 ATCATCGAGCAGCAGCAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCCC	NESULT 2 Sequence 41, Application US/10190435 Sequence 41, Application US/10190435 Sequence 41, Application US/10190435 Sequence 51, Application US/10190435 Sequence 51, Application US/10190435 Sequence 51, Application US/10190435 APPLICANT: UNAN. SERIESTERIES, Season 4 APPLICANT: UNAN. SERIESTERIES, Season 6 APPLICANT: UNAN. SERIESTERIES, Season 6 APPLICANT: UNAN. SERIESTERIES, Sequence 7 FILLS OF INVESTION: DOLYMPLEDIDES FOURTERIESS AND USES THEREOF FULLS OF INVESTION: DOLYMPLEDIDES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES FOURTERIES F

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                                                                                                                                                                                                                                                                                                    DB 16;
                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: p2Pol.opt.YMM_C
US-10-190-305A-37
                                                                                                                                                                                                                                                                                                 Query Match 99.4%; Score 2443.4; Best Local Similarity 100.0%; Pred. No. 0; Matches 2444; Conservative 0; Mismatches
FILE REFERENCE: 2302-18702 / 18702.002
CURRENT PEPLICATION NUMBER: US/10/190,305A
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 2445
                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-100-305A-37

Sequence 37, Application US/10190305A

Sequence 37, Application US/10190305A

Publication No. US20030198621A1

GENERAL INFORMATION:

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: LIAM, Ying

TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
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APPLICANT: ZUR MEGGGG, Jan
APPLICANT: ZUR MEGGGG, Jan
APPLICANT: Barnett, Susan W.
APPLICANT: Barnett, Susan W.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
CURRENT PILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 2463
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US-10-190-435-10
US-10-190-435-10
Sequence 10, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LINR MEGEDE, Jan
APPLICANT: LIAN, Ying
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APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REPERBYCE: PP181313.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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99.9%; Pred. No. 0;
ive 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.9
Matches 2436; Conservative
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Db 3707 TGATCAAGAAGGAGAAGCTGTACCTGAGCTGGCCCCCCCC	RESULT 8 US-10-190-435-58 Sequence 58, Application US/10190435 Publication No. USZ0030143248A1 Sequence 58, Application US/10190435 Publication No. USZ0030143248A1 APPLICANT: ZUR MESEDE, Jan APPLICANT: BARNETT, Susan W. APPLICANT: DAINETTON: POLYPETTIDES, POLYPETTIDES AND USES THEREOF TITLE OF INVENTION: POLYPETTIDES, POLYPETTIDES AND USES THEREOF CURRENT FILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 319 SEQ ID NO S: 319 LENGTH: 5184 TYPE: DNA ORGANISM: Artificial Sequence FRANTURE: PRANTURE: OTHER INFORMATION: Description of Artificial Sequence: TatRevNefgagCpollna C US-10-435-50 Query Match Best Local Similarity 99.9%; Pred. No. 0; Matches 2436; Conservative 0; Mismatches 2; Indels 0; Gaps ON 14 TGGCCGAGGCCATGAGCCACAGGCCCACACCCCAGGCCACACCCCACACCCCACACCCCCACACCCCCACACCCCC	Db 2801 AGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGCCAAGGAGGGCCCACATCGCCCGCA 2860 Oy 134 AGGCCCCCCCCCCCCAAGAGGCCTCCTCCACCGCAAGGAGGCCCACATCGCCCCCAATGA 193 Db 2861 ACTGCCCCCCCCCCAAGAAGGCCTGCTGCAAGAGGGCCCCCCAGATGA 2920 Oy 194 AGGACTGCACCCGACCCCAACTTCTTCCCCCAAGAGGCCCTTCCCCCAGATGA 2920 Oy 254 AGGCCCGCGAGCGCCAACTTCTTCCGCGAGGACCTTCCCCCAGGCA 2980 Oy 254 AGGCCCGCGAGTTCCCCAACAGCAACACCCCACCAGCCCACCAGGCA 2980 Oy 254 AGGCCCGCGAGTTCCCCAACAGCACACACACCCCACCAGCCCCCCAGGCA 2980 Oy 254 AGGCCCGCGAGTTCCCCAACAGCACACACACCCCACCAGCCCCCCAGGCA 2980 Oy 314 AGGTCCGCGGAGTTCCCCAGCGAGCAGCCGCCAACAGCCCCACAGCCCCCTGAACT 3100 Oy 314 AGGTGCGCGGCGACACACCCCCGCAGCGCCCAACAGCCCCCTGAACT 3100 Oy 374 TCCCCCAAAACCCCCGCAGCGCCCCCTGGTGAGCACCCCTGAACT 3160 Oy 374 TCCCCCAAAACCCCCTGTGGCAGCCCCTGGTGAGCACCCTGAACT 3160 Oy 374 TCCCCCAAATCACCCTGTGGCAGCCCCTGGTGAGCAGCCCCTGAACT 3160 Oy 374 TCCCCCAAATCACCCTGTGGCAGCCCCTGGTGAGCAGCCCCTGAACT 433 Db 3101 TCCCCCCAAATCACCCTGTGGCAGCCCCTGGTGAGCAGCCCCTGAACTCA 3160 Oy 434 AGGAGGCCCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGCCCCTGAACT 3160 Oy 434 AGGAGGCCCTGTGGCAGCCCCCTGGTGAGCATCAAGGTGGCCCCTGAACT 3160 Oy 434 AGGAGGCCCTGTGGCAGCGCCCCTGGTGGAGCATCAAGGTGGCCCCTGAACCCCTGAACTCA 433 OY 434 AGGAGGCCCTGTTGGCAGCCCCCTGGTGGAGCATCAAGGCTGCCCCTGAACCCCTGAACCCCCTGAACACTTGCCCCCTGAACACTTGCCCCTGAACACTTGCCCCTGAACACTTGCCCCCTGAACACTTGCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCTGAACACTTGCCCCCTGAACACTTCCCCCAAACCCCCTGAACACTTGCCCCCCCTGAACACTTGCCCCCTGAACACTTGCCCCCTGAACACTTCCCCCAAACCCCCTGAACACTTCCCCCAAACACCCCCCCC

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, OTHER INFORMATION: Description of Artificial Sequence:

, OTHER INFORMATION: TatRevNefgagCpolIna C
US-10-190-305A-82
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: 2302-18702 / 18702.002
CURRENT APPLICATION NUMBER: US/10/190,305A
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 82
LENGTH: 5184
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.9%;
Matches 2436; Conservative (
                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-190-305A-82
Sequence 82, Application US/10190305A
; Sequence 82, Application US/10190305A
; Publication No. US20030198621A1
; GENERAL INFORMATION:
; APPLICANT: SUR MEGEDB, Jan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
    GCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCG
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10	1394 AGCTGCCCGAGAAGGGAGCCGGACCATCCAGAAGCTGGTGGCCAGCAGGAAGCTGA 1451

	1261 CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGGGCTTCACCACCCCCGAC 1320 	1321 AAGAAGCACCGGAGAGCCCCCCTTCCTGCCCATCGAGCTGCACCCCGACAAG 1374 	S TGGACCGTGCAGCCCATCGAGCTGCCCGAGAGGAGGCTGGACCGTGAACGACATCCAG 1 	0 - 0	1495 CTGTGCAAGCTGCTGCGGGGCCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG 1554 	5 GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGGCTGTAC 1	1615 TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGAGGGCCACGACCAGTGGACC 1674 	1675 TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGCAAGTACGCCAAGATGCGC 1734 	1735 ACCGCCCACACCAACGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG 1794	ניז — ניז	1855 GAGACCTGGTGGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1914 	1915 ACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGCAGCCCATCATCGGCGCCGAG 1974	CTACGTG CTACGTG	2035 ACCGACCGGGCGGCGAGAAGATCGTGACCTGACCGACCACCAACCA	2095 CTGCAGGCCATCCAGCTGGCCCTGCAGACAGCGCGCGCGGCGAGGTGAACATCGTGACCGAC 2154	2155 AGCCAGTACGCCTGGGCATCATCCAGGCCCAGCCGACAAGAGCGAGAGCGAGTGTG 2214	2215 AACCAGATCATCGAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC 2274	2275 CACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG 2334
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; OTHER INFORMATION: Description of Artificial Sequence: PR975(+)
US-09-899-575-30
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ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 2469
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                                    TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGGAGCAGGACC
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Publication No. US20030223961A1

GENERAL INFORMATION:

APPLICANT: Zur Megede, Jan

APPLICANT: Barnett, Susan W.

APPLICANT: Egnelbrecht, Susan W.

APPLICANT: Paneburg, Estrelita Janse

TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C

TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: PP01631.102

CURRENT APPLICATION NUMBER: 08/09/899,575

CURRENT FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 09/475,704
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Qy 2029 TACGRAGACCTTCTACGTGGACGCCCCCCAACCGCGAACCCAAGATCGCAAGGCCGGC 2028 Db 1981 GCCGAGACCTTCTACGTGGACGCCCCAACCGCCAACACACAC	RESULT 13 US-10-190-435-13 US-10-190-435-13 i Sequence 13, Application US/10190435 ; Publication No. US20030143248A1 ; Sequence 13, Application No. US2030143248A1 ; GENERAL INCORMATION: APPLICANT: ZUR MAKEDES, Jan APPLICANT: ALAN, TING APPLICANT: LIAN, TING APPLICANT: ENCELBENCH, Susan APPLICANT: ENCELBENCH, Susan APPLICANT: ENCELBENCH, Susan APPLICANT: MAN ENEMBENCH, SUSAn APPLI
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1214 ACCIDENCE CONTRIBUTION
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                                                                                         CAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATC
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                               CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGCATCGGCGGCGCTTCATCAAGGTGCGC
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ACGAGCAGATCGACAAGCTGGTGAGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGCCA
             TCGATGGCGCCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCC
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Publication No. US2030143248A1

GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: WAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT PILLING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 2457
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US-10-190-435-45
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                                                                                                              Query Match 97.8%; Score 2403.4; Best Local Similarity 99.3%; Pred. No. 0; Matches 2439; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: p2Polopt_C US-10-190-305A-39
                                                                                                                                                               Length 2457;
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Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SCOTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 2457
TYPE: DNA
CORGANISM: Artificial Sequence
FRATURE:
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Best Local Similarity 99.3
Matches 2439; Conservative
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Publication No. US20030198621A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FOLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
TITLE OF INVENTION: FOLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: 2302-18702, 18702.002
CURRENT APPLICATION NUMBER: US/10/190,305A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATCTACCAGTACATGGACGACCTG
                   GCCGAGCTGGACCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCCGTGCACGGCGTGTAC
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                                                                                                                      TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC
                                                                                                                                     TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC
                                                                                                                                                                              ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG
                                                                                                                                                                                                                                     AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
                                                                                                                                                                                                                                                      AGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
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US-10-190-305A-39
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0y 1975 ACCTTCTACGTGGACGGCCCAACCGGAGCCCAAGATCGGCAAGGCCGCTACGTG 2034 1981 ACCTTCTACGTGGACGCCGCCAACCGCGAGACCAAGACGCGCGCTACGTG 2040 1981 ACCGACCGGGCGCCGCCCAACCGCGAGACCAACCAACACACGTG 2040 2035 ACCGACCGGGGCGCGCCGCCCCCCCCCCCCCCCCCCCC	Search completed: June 2, 2005, 04:23:48 Job time : 1415.9 secs
841 CCCGTGTTCGCCATCAAGAAGACACCAAGTGGCGCAAGCTGGTGGACTTCCGC 900 907 GAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCCGCC 966 908 GAGCTGAACAAGCGCACCCAGGACTTCTGGAGGTGCAGCTGGGCATCCCCCACCCCCCC 960 967 GGCCTGAACAAGAAGAAGACTTCTGGAACTTCTGGAGCTGCAGCTTCCCCCCCC	1315 TGGACCCTGCAGCCCATCGACCTGCCCGAGAAGGAGAGCTGGACCCTGAACGACATCCAG 141 1381 TGGACCCTGCAGCCCATCCGACAAGGAGAGGTCGACCCTGAACGACACACTCCAG 1440 1435 TTGGACCGTGCAGCCTGACCCGAAACGAGACTCCAGCTGAACGACGACGAGGAGTCGACCCCGCAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCGAGGAGGTCGACCCCCGAGGAGGTCGACCCCAGAGGAGGTCGACCCCCGAGGAGGTCGACCCCAGAGGAGGTCGACCCCCAGAGGAGGTCGACCCCCAGAGGAGGTCGACCCCCAGAGGAGGTCGACCCCAGAGGAGGTCGACCCCAGAGGAGGAGCTGACCCCAAGACCCCAAGACCCCCAAGACCCCAAGACCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCAACACCCCCAAGACCCCCAAGACCCCCAAGACCCCCAAGACCCCCC

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nucleic search, using sw model OM nucleic - Run on:

May 31, 2005, 23:20:00; Search time 1267.33 Seconds (without alignments) 11504.726 Million cell updates/sec

Title: Perfect score:

US-09-610-313B-31 2463

1 gtcgacgccaccatggccga.......ggggctagcaccggtgaattc 2463 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 16Dec04:* geneseqn1980s: Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID .	G
-	2463	100.0	2463	9	ABL39960	Ab13996
8	2463	100.0		12	ADM73765	Adm737
e	2455.4	99.7		80	ACA03547	Aca0354
4	2455.4	99.7		10	ADC13265	Adc132
w	2442.2	99.5	2469	9	ABL39959	Ab13995
9	2442.2	99.5	2469	12	ADM73764	Adm737
r	0,000	0			12000104 2	שטטכנאג

Description	Abl39960 Synthetic	Adm73765 HIV-1 pol	Aca03547 Synthetic	Adc13265 DNA of HI	Abl39959 Synthetic	Adm73764 HIV-1 pol	Abl39961 Synthetic	Adm73766 HIV-1 pol	Aca03548 Synthetic	Adc13266 DNA of HI	Aca03546 Synthetic	Adc13264 DNA of HI	Adc13230 DNA of HI	Adc13231 DNA of HI	Adc13232 DNA of HI	Aca03591 Synthetic	Adc13279 DNA of HI	N.	Adc13236 DNA of HI	Aca03521 Synthetic
ID .	ABL39960	ADM73765	ACA03547	ADC13265	ABL39959	ADM73764	ABL39961	ADM73766	ACA03548	ADC13266	ACA03546	ADC13264	ADC13230	ADC13231	ADC13232	ACA03591	ADC13279	ADC13234	ADC13236	ACA03521
DB	9	12	80	10	9	12	9	12	80	10	8	10	10	10	10	8	10	10	10	œ
Çuery Match Length DB	2463	2463	2457	2457	2469	2469	2457	2457	2457	2457	2445	2445	3930	3930	3930	5184	5184	3531	3537	5145
Query Match	100.0	100.0	99.7	99.7	99.2	99.5	98.9	98.9	98.7	98.7	98.4	98.4	98.1	98.0	98.0	98.0	98.0	96.8	96.7	96.7
Score	2463	2463	2455.4	2455.4	2442.2	2442.2	2436.2	2436.2	2430.2	2430.2	2422.6	2422.6	2415.6	2414	2414	2414	2414	2383.6	2382	2381
esult No.	-	~	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	11	18	19	20

DNA	Adc13235 DNA of HI		Adc13269 DNA of HI	Aca03550 Synthetic	Adc13268 DNA of HI	Aca03549 Synthetic	Adc13267 DNA of HI	Aca03542 Synthetic	Acc78506 HIV p2Pol		Acc78507 HIV p2Pol	Aca03541 Synthetic	Acc78505 HIV p2Pol	Acc78488 HIV GagPo	Acc78489 HIV GagPo	Aca03522 Synthetic	Adc13238 DNA of HI	Acc78484 HIV GagCo	Acc78485 HIV GagCo	Acc78486 HIV GagCo	Aca03584 Synthetic	Acc78529 HIV TatRe	Aca03592 Synthetic	Adc13280 DNA of HI
ADC13233	ADC13235	ACA03551	ADC13269	ACA03550	ADC13268	ACA03549	ADC13267	ACA03542	ACC78506	ACA03543	ACC78507	ACA03541	ACC78505	ACC78488	ACC78489	ACA03522	ADC13238	ACC78484	ACC78485	ACC78486	ACA03584	ACC78529	ACA03592	ADC13280
10	10	œ	2	æ	10	œ	10	æ	œ	æ	œ	œ	æ	œ	œ	œ	10	80	æ	8	80	80	æ	10
5145	3538	3607	3607	3624	3624	3597	3597	2466	2466	2472	2472	2460	2460	3564	3564	4716	4716	3999	3999	3999	5283	5283	4713	4713
96.7	96.3	94.3	94.3	94.3	94.3	93.6	93.6	87.0	87.0	86.2	86.2	85.9	85.9	85.8	82.8	82.8	85.8	85.7	85.6	85.6	85.6	85.6	85.6	85.6
2381	2371	2322.6	2322.6	2322.6	2322.6	2304.4	2304.4	2142	2142	2122.8	2122.8	2115.2	2115.2	2114.2	2114.2	2113.6	2113.6	2109.8	2108.2	2108.2	2108.2	2108.2	2108	2108
21	22	23	24	25	56	27	58	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ABL39960 standard; DNA; 2463 RESULT 1 ABL39960

BP.

ABL39960;

(first entry) 15-MAY-2002

Synthetic construct PR975YM SEQ ID NO:31.

Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.

Human immunodeficiency virus; type C. Synthetic.

WO200204493-A2.

17-JAN-2002.

05-JUL-2001; 2001WO-US021241.

05-JUL-2000; 2000US-00610313.

(CHIR) CHIRON CORP. (UYST-) UNIV STELLENBOSCH.

Ε. Van Rensburg Engelbrecht S, Barnett SW, Zur Megede J,

WPI; 2002-154920/20.

New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.

Claim 1; Fig 9; 233pp; English.

The present invention describes expression cassettes comprising a polymucleotide sequence encoding a polymeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gay, Pol, Vif, Vpr, Tat, Rev, Vpu, Bnv or Nef (I). (I) have immunostimulant activity and can be used in gene therapy.

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useful in applications including DNA
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DNA HIV He He In Of	, 0 s	AG 60 	GC 120 	AG 180	CC 240	CC 300	AG 360 	TG 420 	AG 480 	AG 540 	TG 600	dc 660 GC 660	TG 720 - TG 720	CC 780	AC 840 	AC 900
ful in applications : cell lines, and prodi re particularly useft ons. ABL39942 to ABL es used in the exemp	163; DB 6; Len 5.3.9e-297; ches 0; Ind	GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCTGATGCAGGCAG	CGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 	CACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG 	GGCCACCAGATGAAGGACTGCACCGAGGGCCAACTTCTTCCGGGAGGACTGGC 	CAGGGCAAGGCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCAC 	CGCGGCGACAACCCCGCAGCGAGGCCGGGCGCCGAGCGCCAG	GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTG 	GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGCACGTGCTGGAGGGG 	atgagcctgcccggcaagtggaagcccaagatgatcggcggcatcggcggcttcatcatgag 	GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGCCATCGGCACCGTG 	CTGAITCGGCCCCACCCCGTGAACAICAITCGGCCGCAACAIGCTGACCCAGCTGGGCTG 	ACCTGAACTTCCCCATCAGCCCCATGAGACCGTGCCCGTGAGCTGAAGCCCGGCATG	GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACGGC 	ATCTGCGAGGAGATGGAGGAGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 	aacaccccgtgttcgccatcaagaagacagcaccaagtgggggaagggcgaagctggtgggc
type C polynucleotides are u ation, generation of packagin proteins. The polynucleotides and and mimunisation applica to ABB06215 represent sequesent invention	100.0%; imilarity 100.0%; Conservative	1 GTCGACGCCACCATGCCGAGGCCATG				TTCCCC	AGCCGCGAGCTGCAGGTG									
CC The HIV CC immunis CC Type C CC Thereno	3es Jat	දුරු අ	Qy 61 Db 61	Qy 121 Db 121	Qy 181 Db 181	Qy 241 Db 241	Qy 301 Db 301	Qy 361 Db 361	Oy 421 Db 421	Qy 481 Db 481	Qy 541 Db 541	Qy 601 Db 601	Qy 661 Db 661	Qy 721 Db 721	Qy 781 Db 781	Oy 841 Db 841

ò	901 TICCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGCGGCATCCCCCAC 960
qq	901 Trocacadaradacacacacadaactrotagaagagagagagagaagaacaracaaa 960
ò	961 CCGCCGGCCGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGACGCGACGCCTACTTC 1020
дg	1 cccgcccgccrtgaagaagaagaagagcgrgaccgrgcrtggacgrgacgacgacgrcracrrc
ò	1021 AGCGTGCCCCTGGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1080
qq	1 Accertecectrocacados controcacados acontrocamentos de la Accepta de la
ò	1 AAGAGACCCCGGGATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC
qq	1 AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC
ò	1141 CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCTTCCGCGCCCGCAACCCC 1200
QQ	CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC
δ	GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC
qq	GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC
λ	CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGCTGGGGCTTCACCACCCCCGAC
Dp	CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCCTGGGGCTTCACCACCCCCGAC
δ	ABGAAGCACCCCAAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCCGACAG
οp	AAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAG
δ	TIGACCGTIGCAGCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACGACGACTCCAG
Dþ	TGGACCGTGCGCCCATCGACTGCCCGAGAGGAGGAGCTGGACCGTGAACGACATCCAG
Š	AAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG
qq	AAGCTGGTGGCGAAGCTGAACTGGGCCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG
δλ	CTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGGGGGG
Ωp	CTGTGCAAGCTGCGCGCGCGAAGGCCCTGACCGACTGTGGTGCCCTGACCGAGGAG
δλ	GCCGAGCTGGAGCTGGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTTAC
οqα	GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCCGTGCACGGCGTGTAC
δλ	1621 TACGACCCAGCAAGAACTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC 1680
QQ	TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC
ò	TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC
qq	TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC
Š	ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG
qa	ACCECCACACCAACGACGAGGAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG
δ	AGCATCGIGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGCTGG
qa	AGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
δ	1861 GAGACCTGGTCGACTACTCGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1920
ορ	1861 GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC 1920
ζ	ACCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGAAGAAGCCCATCGTCGGCGCCGAG
qq	921 ACCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG
δλ	ACCTTCTACGTGGACGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG

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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence turther comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGGGAGCAGAACCGCGCCAACAGCCCCACC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCACCAGATGAAGGACTGCACCGAGCCCAACTTCTTCCGCGAGGACCTGGCC
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CCTTAC CCTTAC CCTTAC CCCCCCCCCCCCCCCCCC	1411 AAGCTGGTGGGCAAGCTGAACTGGCCAAGTTCTACCCGGCATCAAGGTGCGCCAG 1500 1411 AAGCTGGTGGCCAAGGTGCGCAGCCAGCTGACCGGCATCAAGGTGCGCCAG 1501 1411 AAGCTGGTGGCCAAGGTGCGCAGCCAGCCAGCTCACCCGGCATCAAGGTGCGCCAG 1500 1501 CTGTGCAAGGTGCGCCACGCCAGCCCTGACCGAGCCCTGACCGAGGAG 1500 1501 CTGTGCAAGGTGCCCGAAGGCCCTGACCGACACGCCCTGACCGAGGAG 1501 1501 CTGTGCAAGGTGCCCGAGAGCCCTGACCGACCCGAGGAG 1501 1501 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601 1601

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The invention describes a synthetic polymucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polymucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polymucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV. The gene delivery vector comprising the polymucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide New synthetic polynucleotides encoding antigenic HIV type B and/or type (polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans. Example 1; Fig 35; 262pp; English. Lian SW, Barnett (CHIR) CHIRON CORP 2003-221602/21 Zur Megede J, WPI;

Sequence 2457 BP; 564 A; 835 C; 758 G; 300 T; 0 U; 0 Other;

120 180 240 300 300 360 420 420 480 480 540 540 900 900 CTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC 660 9 CACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGAAG TTCCCCCAGGGCAAGGCCCGCGGGTTCCCCAGCGAGAGAGCCGCGCCAACAGCCCCACC GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAG Gregaegecargaegaggeargaegecaggecaggecaacarcargargeag CGCAGCAACTTCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC CGCAGCAACTTCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGGC CACATCGCCCGCAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG GGCCACCAGATGAAGGACTGCACCGAGCGCCAAGCCAACTTCTTCCGCGAGGACCTGGCC TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACC AGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCAGCGAGGCGCGGCCGAGGCGCCAG GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCCTGGTGAGCATCAAGGTG GGCACCCTGAACTTCCCCCCAGATCACCCTGTGGCGCCCCCCTGGTGGCGC GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAG GGCGGCCAGATCAAGGAGGCCCTGCTGGCCACCGCCGCCGACGACGACGACGACGACGAGGAG ATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCGGCGCGCATCGGCGCCTTCATCAAG ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGCGCTCGTCCATCAAG GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG GTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG Gaps 99.7%; Score 2455.4; DB 8; Length 2457; larity 100.0%; Pred. No. 3.5e-296; Conservative 0; Mismatches 1; Indels 0; Query Match Best Local Similarity Matches 2456; Conserv Н 61 241 601 19 121 181 181 241 301 301 361 361 421 121 481 481 541 541 8 6 8 6 6 6 6 6 6 6 셤 Š 음 상 음 8 8 셤

1080 1260 1440 1020 1020 1140 1380 1500 1560 1620 1620 1680 1740 720 720 780 780 840 840 900 960 960 1021 AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC CTGTGCAAGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC GACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCC 781 Arcreceaegagargaagaagaagaggcaagarcaccaagarcegcccceaeaaccccrac 841 AACACCCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGGACGTGGACGTGGGCGACGCCTACTTC 1021 AGGGTGCCCCTGGAGGACTTCCGCAAGTACACGCCTTCACCATCCCCAGCATCAAC 1081 AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCAGC 1201 GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC GACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACGCC ATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 901 TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTC **AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC** GAGATCGTGATCTACCAGGCCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAC 1261 CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGCGCTTGGGCCTTCACCACCCCCGAC AAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCCGACAAG 1321 AAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCGACAAG TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAG AAGCTGGTGGCCAAGCTGAACTGGGCCAGCCAGATCTACCCCCGGCATCAAGGTGCGCCAG CTGTGCAAGCTGCTGCGCGCGCGCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAG GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTAC GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGCGTGTAC TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACC TACGACCCCAGCAAGGACCTGGTGGTGGCCGAGATCCAGAAAGCAGGGCCACGACCAGTGGACC CGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCG 1141 1081 1141 1441 1681 991 661 721 721 781 841 901 961 961 1201 1261 1321 1381 1381 1441 1501 1501 1561 1561 1621 1621 501 요 셤 셤 셤 셤 ద g g ò 8 ò 셤 8 g ò ద 8 ò ò δ 셤 ठ g 셤 Š 셤 셤 ò 셤 ઠે ò ò ઠે Š ò

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TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCCAAGTACGCCAAGATGCGC 1740
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                           ACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAG
                                                            AGCATCGTGATCTGGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGG
                                                                                               GAGACCTGGTGGACGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC
                                                                                                                                                               ACCTICTACGTGGACGCCCCCCCACCCGGAGACCAAGATCGGCAAGACCGGCTG
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The invention relates to a novel expression cassette comprising a polymorleotide sequence encoding a polypeptide including an HIV Gag, Int, Nef, pismaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscosally, intranssally, subcutaneously, intradermally, transdermally, intraveginally, intravectally, orally or intravenously. The expression cassette is useful for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymucleotide sequence represents the DNA of an HIV Type C related sequence of the invention.
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                                                                                                                                                                                                                                                             The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL33942 to ABL40054 and ABB06225 represent sequences used in the exemplification of
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Pred. No. 1.5e-294;
0; Mismatches 3;
                                                                                                                          Engelbrecht S,
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                              05-JUL-2001; 2001WO-US021241
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                                                                                 (CHIR ) CHIRON CORP. (UYST-) UNIV STELLENBOSCH
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Matches 2460; Conservative
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99.2%; Score 2442.2; DB 12;
Best Local Similarity 99.6%; Pred. No. 1.5e-294;
Matches 2460; Conservative 0; Mismatches 3; If
     Human immunodeficiency virus 1.
                                                                                                 05-JUL-2000; 2000US-00610313
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RENSBURG E J V.
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BARNETT S W.
ENGELBRECHT (
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                           US2003223961-A1
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HIV-1; gene; ds; HIV pol; immune response; DNA immunisation;
HIV type C protein; immunostimulant.
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The invention relates to an expression cassette comprising a polymucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polymucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polymucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                                                          New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
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EJV;
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Engelbrecht S,
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Qy 1495 CGCCAGCTGTGCAAGCTGCTGCGGGCCCCAAGGCCCTGACCGACATCGTCCCCTGACC 1554 Db 1501 CGCCAGCTGTGCAAGCTGCTGCGGGGCCCTGACCGACATCGTGCCCCTGACC 1560 Qy 1555 GAGGAGGCCGAGGCTGGCCGAGATCCTGCGCGAGATCCTGCGCGGGCCCTGCACGGC 1614 Db 1561 GAGGAGGCCGAGGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCACGGC 1614 Db 1615 GAGGAGGCCGAGGCTGGCCGAGAACCGCGAGATCCTGCGCGAGGCCCGTGCACGGC 1620 Qy 1615 GTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCACGACCACGACCAGGCCCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCACGACCCACGACCACGACCACGACCCACGACCACC	OY 1675 TGGACCTACCAGAGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAG 1734	Oy 1795 ATGAGAGCATCGTGATCTGGGGCAAGTTCCGCCTGCCCATCCAGAAGGA 1854	1915 GTGAACACCCCCCCCCGGGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGC 197	1981 GCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGGGGACCAAGATCGGCAAGGTCGGC 20 2035 TACGTGACCGACCGGGGGCGGAGATCGTGAGGCTGACCGAGACCACCAACAGAAG 20 2041 TACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCACCAGAAG 20	Qy 2095 ACCGAGCTGCAGGCCTGCAGGACCAGGCAGCAGGAGGTGAACATCGTG 2154		23 24 24	Qy 2395 GACCTGTACGTGGGCAGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACC 2454 Db 2401 GACCTGTACGTGGGCGGCCCTAGGATCGATTAAAAGCTTCCGGGGCTAGCACC 2460 Qy 2455 GGTGAATTC 2463 Db 2461 GGTGAATTC 2469	RESULT 7 ABL39961 ID ABL39961 standard; DNA; 2457 BP. XX
421 GGCGGCCAGATCAAGGAGCCCTGCTGGACCCCGGCGCCGACGACGACGTGCTGGAGGAG 480 [CTGATCGGCCCCACCCGTGAACATCATCGGCCGCAACATGTGAACCCAGCTGGCGCTGCTGCTGTTTTTTTT	GACGCCCCAAGGTGAAGCAGTGGCCCCTGAGAGAGATCAAGGCCCTGACCCCGCC 78 GACGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAAAGATCAAGGCCCTGACCGCC 78 GACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAAAGATCAAGGCCCTGACCGCC 78 ATCTGCGAGGAAGATGGAGAGAAGAAGAATCACCAAGATCGGCCCCGAGAACCCCTAC 84	regac 90 regac 90			1081 AACGAGACCCCGGCATCCGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGC	GAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGCC 136 CAGCACCGCGCCAAGATCGAGAGCTGCGCAAGCACCTGCTGCGGCTGGGGCTTCACCACC 131.	CCCGACAGGAGGACCCCCTTCCTGGGATGGGTACGGCTACGAGGTGCCCCCCCC	1435 ATCCAGAAGCTGGGCAAGCTGAACTGGGCCAGATCTACCCGGCATCAAGGTG 1494

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HI type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of
                                                                                                            Human immunodeficiency virus type C; antigenic HIV type C protein;
immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef;
immunostimulant; gene therapy; gene; ds.
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Pred. No. 8.3e-294;
0; Mismatches 3; Indels 6;
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                                                                           Synthetic construct PR975YMWM SEQ ID NO:32
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                                                                                                                                                                                     Human immunodeficiency virus; type C
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Best Local Similarity 99.6%;
Matches 2454; Conservative C
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UNIV STELLENBOSCH
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                                  AAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAG 1500
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TGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAG 1434
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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence turther comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
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HIV type C protein; immunostimulant.
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99.6%; Pred. No. 8.3e-294;
iive 0; Mismatches 3;
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                                 ADM73766 standard; DNA; 2457
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Matches 2454; Conservative
                                                                                                                                 HIV-1 polynucleotide #9.
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BARNETT S W.
ENGELBRECHT S
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1975 ACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTG CACAAGGGCATCGGCCGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG GCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTAC TACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGC CTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACGAC AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
                                                                              TACGTGGGCGGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGTGAA
                                                     TACGTGGGCAGCGGCCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGTGAA
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Pred. No. 4.6e-293;
0; Mismatches 3; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2457 BP; 568 A; 830 C; 758 G; 301 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic DNA ecoding immunogenic HIV peptide #31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ×
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                                                                                                                                                                                                                                                                                                                 BP.
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31-AUG-2001, 2001US-0316860P.
16-JAN-2002, 2002US-0349793P.
16-JAN-2002, 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                 ACA03548 standard; DNA; 2457
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llarity 99.6%;
Conservative
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Best Local Similarity
Matches 2448; Conserv
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                                                                                                                                                  TTC 2463
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The invention relates to a novel expression cassette comprising a polynuclectide sequence encoding a polyneptide including an HIV Gag, Ent, Nef, piStnaseH, Pol, Tat, Prot, or Rev Polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranssally, intradermally, transdermally, intraveginally, intravectally, orally or intravenously. The expression cassette is useful polymentation, generating packaging cell lines and producing HIV polypeptides. This polymuclecide sequence represents the DNA of an HIV Type C related sequence of the invention.
                                                                                                                        AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCC
                   AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGCCGCC
                                                             CACAAGGGCATCGGCGCCAACGAGATCGACAAGCTGGTGAGCCAAGGGCATCCGCAAG
                                                                                         CACAAGGGCATCGGCGAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, piSRnaseH, Pol, Tat, Prot, or Eve polypeptide, useful for immunization, or generating packaging cell lines.
                                                                                                                                                                                       TACGTGGGCGCGCGCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT
                                                                                                                                                                                                        TACGTGGGCAGCGGCCCTAGGATCGATTAAAAACTTCCCGGGGGCTAGCACCGGT
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Pred. No. 4.6e-293;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              cassette; HIV Gag; Env; Int; Nef; p15RnaseH;
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                                                                                                                                                                                                                                                                                                                                                                                               of HIV construct p2Pol-opt_C SEQ ID NO 45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 42; 301pp; English.
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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Matches 2448; Conservative
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7 GCCACCATGGCCGAGGCCATGAGCCAGCGCCAACATCCTGATGCAGCGCAGC 66	187 CAGATGAAGGACTGCACCGAGCCCAACTTCTTCCGCGAGGACCTGCCC 246		CAGATCAAGGAGCCCTGCTGGACACCGGCGCCGACGCGCGCG		GGCCCCACCCCGTGAACATCATCGGCGCAACATGCTGACCCAGGTGGGCTGCACCCTG		GAGGAGATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACACCCC 84	CCCGTGTTCGCCATCAAGAAGAACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGC 90	GAGCTGAACCAGCGCCCCGGGACTTCTGGGAGCTGGGCGGGGCTGGGCCCCCCCC	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New synthetic polynucleotides encoding antigenic HIV type B and/or type C bytypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
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CACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAG
                                                     AACCAGATCATCGAGCAGCTGATCAAGAAGAGGAGAAGGTGTACCTGAGCTGCCCGCC
                                                                             AACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAAGGTGTACCTGAGCTGGGTGCCCGCC
                                                                                                                        CACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGGCATCCGCAAG
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31-AUG-2001, 2001US-0316860P.
16-JAN-2002, 2002US-0349793P.
16-JAN-2002, 2002US-0349871P.
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  Length 2445;
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     DB 8;
  Score 2422.6; DB 8;
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Best Local Similarity 99.6%;
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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag. Env., Int., Nef., plStnaseH, Pol., Tat., Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramuscally, intransally, subcutaneously, intradermally, transdermally, intravaginally, intravectully, orally or intravenously. The expression cassette is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tat; Prot;
                               GCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAG
                                                                       GGCATCGGCGGCAACGAGCAGATCGACAAGCTGAGCAGAGCAAGGGCATCCCCAAGGTGCTG
                                                                                                                                                                                             GGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG
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                                                                                                                                                                                                                                                                                                                  GGCAGCGGCCCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT
                                                                                                                                                                                                                                                                                                                                  GCCAGCGGCCGCCTAGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGT
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Rev; HIV type C; gene therapy; vaccine; immunisation; HIV;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intraveginally, intrazectally, orally or intravenously. The expression cassette is u for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymucleotide sequence represents the DNA of an Type C related sequence of the invention.
                                                                                                                                                                                                                                98.1%; Score 2415.6; DB 10; Length 3930; llarity 99.6%; Pred. No. 2.8e-291; Conservative 0; Mismatches 4; Indels 6; C
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	RESULT 14 ADC12231 ED ADC12231 standard; DNA; 3930 BP. XX ADC13231; XX ADC13231; XX ADC13231; XX BON of HIV construct GagComplPolmutAtt_C SEQ ID NO 10. XX EVERSION CASSELTE; HIV Gag; Env; Int; Nef; plSRnaseH; Pol; Tat; Prot; XX C ADC1304620-A2. XX Human immunodeficiency virus. XX Human immunodeficiency virus. XX D 16-JAN-2003. XX C -JUL-2001; 200118-03193P. XX C -JUL-2001; 200118-03193P. XX C -JUL-2001; 200118-03193P. XX C -JUL-2001; 200118-03198P. XX C -JUL-20
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int, Nef, plsRnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is u for immunisation, generating packaging cell lines and producing HIV polypeptides. This polymucleotide sequence represents the DNA of an Type C related sequence of the invention.
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                                                                                                                    Length 3930;
                                                                                                  Sequence 3930 BP; 889 A; 1365 C; 1214 G; 462 T; 0 U; 0 Other;
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                                                                                                                   Score 2414; DB 10;
Pred. No. 4.4e-291;
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TGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCCGAGACCTTCTACGTGG
                                                                                                              TGGGCATCATCCAGGCCCAGCACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCG
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                                                                                                                                                                                                                                                                                                                                                                             type C; gene therapy;
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                     standard; DNA; 3930
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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Env Int, Nef, piSRnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutanaeously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is usefu for immunisation, generating packaging cell lines and producing HIV polypeptides. This polynucleotide sequence represents the DNA of an HIV Type C related sequence of the invention.
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Pred. No. 4.4e-291;
0; Mismatches 5;
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2267 TGGAGAAGGAGGCCAAGATCACCAAGATC	854 TCGCCATCAAGAAGAAGGACAGCACCAAC 	914 ACAAGGGACCCAGGACTTCTGGGAGGTC 	974 AGAAGAAGAAGAGCGTGACCGTGCTGGAC 2447 AGAAGAAGAGCGTGACCGTGCTGGAC	1034 ACGAGGACTTCCGCAAGTACACCGCCTTC 	1094 GCATCCGCTACCAGTACAACGTGCTGCCC 	1154 AGAGCAGCATGACCAAGATCCTGGAGCCC 1154	1214 ACCAGGCCCCCTGTACGTGGGCAGCGAC 	1274 AGGAGCTGCGCAAGCACCTGCTGCGCTGC 2747 AGGAGCTGCGCAAGCACCTGCTGCGCTGC	1334 AGGAGCCCCCTTCCTGTGGATGGGCTAC 2807 AGGAGCCCCCTTCCTGCCCAT	1394 CCATCGAGCTGCCCGAGAAGGAGGCTGC 	1454 AGCTGAACTGGGCCAGCCAGATCTACCCC	1514 TGCGCGGCCCAAGGCCTGACCGACATC 	1574 TGGCCGAGAACCGCGAGATCCTGCGCGAA 	1634 AGGACCTGGTGGCCGAGATCCAGAAGCAC 	1694 AGGAGCCTTCAAGAACCTGAAGACCGG 	1754 ACGACGTGAAGCAGCTGACCGAGGCCGTC 	1814 GGGGAAGACCCCCAAGTTCCGCTGCCC 	1874 CCGACTACTGGCAGGCCACCTGGATCCCC

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earch completed: June 1, 2005, 11:33:26 ob time : 1275.33 secs

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Sequence 31 from Patent WO0204493.
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DEFINITION
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KEYWORDS
SOURCE
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RESULT 2 AX455914 LOCUS DEFINITION ACCESSION VERSION	2 4 AX455914 2469 bp DNA linear PAT 06-JUL-2002 ION Sequence 30 from Patent W00204493. DN AX455914 AX455914.1 GI:21714899	8 8 8	661 ACCCTGAACTTCCCCATCGACCCTGCCCGTGAAGCTGAAGCCCGGCATG 720
KEYWORDS SOURCE ORGANISM	synthetic construct ISM synthetic construct other sequences; artificial sequences.	& ga	781 ATCTGCGAGGAGATGGAGAGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTAC 840
AUTHORS TITLE	SS zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, B. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof	ý da	841 AACACCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC 900
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	/note="PR975(+)" /db_xref="taxon:32630" /note="PR975(+)"	λό a	961 CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCTGCTGCACGTGGCGACCCCTACTTC 1020
Okidin Query Best L	ore 2442.2; DB 6; Length 2469;	& a	1021 AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1080 1021 AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCACCATCAAC 1080
Oy Dh	ACCATGGCGG7	ò a	1081 AACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTCCCCAGGGCTGGAAGGGCAGC 1140
3 & 5	GCGCACCACCTTCAAGGCCCCCAAGCGCATCATCAAGGCCTCTCAACTGCGCAAGGGCCAAGGCCCAACTCATCAAGTGCTTCAACTGCGGCAAGGGGCCAAGGCCGCAAGGGCCAAGGGCCAAGGCGCAAGGGCCAAGGGCCAAGGGCCAAGGAAGGCCAAGGAAGGCAAGGAAGGAAGGCCAAGGAAGGAAGAA	& 8	1141 CCCAGCATCTTCCAGAGCAGGATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCACCCC 1200
3 6 8	CACATICACCCCACACCCCCAAACACCCCTCAACTGCTTCAACTGCGGGAAAGAGGGCTTCAACTGCGGGCAAAGAAGGGCTTCAACTGCGGGCAAAGAAGGGCTTCAACTGCGGCAAAGAAGGGCTTCAACTGCGGCAAAGAAGGAAG	& 8	1201 GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCACCTGGAGATCGGC 1254
සී රී සි	GGCCACCAGATGAAGGACTGCCCCCCGCAAGAAGGCTGCTAGAAGTGCGCGCAAGAGCTGCAAGAAGTGCGCAAGAAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGA	& a	1255 CAGCACCGCGCCAAGATCGAGGAGCTGCGCACCTGCTGCTGCTGCTGCGGTTCACCACC 1314
G & A	TICCCCCAGGGCAAGGCCCGCGAGTTCCCCAGGCAGAACGCCGCCAACAGCCCACCCA	& 43	1315 CCCGACAGAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCCCC 1374
8 8 8	AGCGGGAGCTGCAGGTGCGCGGCAAAACCCCCGAGCAGGCGGCCGAGCGCCCAGCAG	ò 8	1375 GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAGGAGGGCTGGACCGTGACGAC 1434
3 & 1	AGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCCCCCCTGGTGAGCTCAGCACCAGCACCAGATGATCACCCTGTGTGAACTTCAACGTGAACTTCAACGTGAACATGAACAACGTGAAACAACAAAAAAAA	ò a	1435 ATCCAGAAGCTGGTGGCCAGCTGAACTGGGCCAGCCAGTCTACCCCGGCATCAAGGTG 1494
g & i	GGCGGCCAGATCTCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTG GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCCGGCCGCCCCCTGGTGAGGTG	& 43	1495 CGCCAGCTGTGCAAGCTGCTGCGGGGCCCAAGGCCCTGACCGACATCGTGCCCCTGACC 1554
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    /organism="synthetic construct"
/mol_type="unassigned DNA"
    /db xref="taxon:32630"
    /note="PR975YMWM"

polypeptides and uses thereof
Patent: WO 0204493-A 32 17-JAN-2002;
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                                      Score 2046; DB 6; Length 2
Pred. No. 1.1e-204;
0; Mismatches 135; Indels
/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="taxon:32630"
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                                                                                                      GCGGCAAGGACGCCACACAAGAAGGACTGCACCGAGCGCCAGGGCCAACTTCTTCCGCG
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 virus-like
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                                                                        Length 2306;
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Expression of HIV polypeptides and production particles
Patent: US 6602705-A 82 05-AUG-2003;
Docation/Qualifiers
1. .2306
                                                                      83.1%; Score 2046; DB 6;
ilarity 93.6%; Pred. No. 1.1e-204;
Conservative 0; Mismatches 135;
                                       /organism="unknown"
/mol_type="genomic DNA"
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Matches 2159; Conserv
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1436 ACANATGRACCTOCACCATCGRACTCACACCACACCACCACCTCACACCTCACACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCT	BD263706 LOCUS BD263706 LOCUS BD263706 DEFINITION Improved expression of HIV polypeptides and production of virus-like particles.
	4280 CCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGGATGGGCTACGAGCTGCACCCCG 4339 1376 ACAAGTGGACCGTGCAGCCGTGCAGCCCGAGAAGGAGGGGTGGACCGTGCACCCCG 4335

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                                                                              AGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGCCAAGATCACCA
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Na Artificial Sequence
PN JP 2002533124-A/73
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PD 08-CCT-2002
PF 31-DEC-1999 JP 2000591193
PR 31-DEC-1999 US 60/114495,01-DEC-1999 US 60/168471 PI KARIN HARTOG,
PL KARIN HARTOG,
PI HONG LIU,CATHERINE GREER,MARK SELBY,CHRISTOPHER WALKER PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P31/18,A61P37/02, PC C12N5/10,
PC C12N7/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC DESCRIPTION OF ARLÍFICIAL SEQUENCE: FS(-).protmod.RTopt(+) FH Ke Location/Qualifiers
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other sequences, artificial sequences.

(bases 1 to 2312)
Barnett,S., megede,J.Z., Srivastava,I., Lian,Y., Hartog,K.,
Improved expression of HIV polypeptides and production of
virus-like particles
Patent: JP 2002533124-A 73 08-OCT-2002;
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/mol_type="genomic DNA"
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ORIGIN Query Match Query Match Best Local Similarity 93.3%; Pred. No. 1.7e-202; Matches 2156; Conservative 0; Mismatches 138; Indels 18; Gaps 3; Qy 170 GCGCAAGGAGGCCACCAGATGAAGGACGACCAGGCCAGCCA	230 AGGACCTACCCCCAGGGAAAGGCCGCGCGGTTCCCCGGGGAGCAGCGCCCCAGCGAGCG	Db 121 ACAGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Db 241 GCCCCTGGTGACCATCAGGATCGGCGGCTCAAGGAGGCGCTCCACGACGCGCG 300 Qy 458 CCGACGACCTGCTGGAGGAGATGGGCTGCCTGCCGGCAAGATGATGG 517 Db 301 CCGACGACACGCTGCTGGAGATGAACCTGCCCGGCAAGTGGAAGCCAAGATGATCG 360 Qy 518 GCGCATCGGCGGCTTCAAGGTGGCCCAGTACGAAGTCCTGATGATCG 577	481 ACCTGATGACCCGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGACGGTGC 698 CCGTGAAGCTGAAGCTGGACGGCCCCAAGGTGAAGCTGCAGGGGG 698 CCGTGAAGCTGAAGCCCGGGCATGGACGGCCCCAAGGTGACGGGGG 698 CCGTGAAGCTGAAGCCGGGGATGGACGGCCCCAAGGTCAAGCAGGCCCCTGACGAGG 758 AGAAGATCAAGGCCCTGACGCCCTTCGCGAGGAGAGGAG	
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PR 31-DEC-1999 US 60/168471 PI
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SUSAN BARNETT, JAN ZUR MEGEDE, INDRESH SRIVASTAVA, YING LIAN, PI
KARIN HARTOG,
PI HONG LIU, CATHERINE GREER, MARK SELBY, CHRISTOPHER WALKER PC
C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61F31/18, A61F37/02, PC
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PC C12N7/00, C12P21/02, C12N15/00, C12N5/00, A61K37/02 CC
Description of Artificial Sequence: PS(-).protmod.RTopt.YMWM PH
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Barnett,S.W., Megede,J., Greer,C. and Selby,M.
Expression of HIV polypeptides and production of virus-like
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Pred. No. 7.1e-202;
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Patent: US 6602705-A 83 05-AUG-2003;
Location/Qualifiers
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/organism="unknown"
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   2275 TTCCCGGGGCTAGCACCGGTGAATTC 2300
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AR373388 1 GI:40075491
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                                                               GCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGA
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Modifications of hiv env, gag, and pol enhance immunogenicity for genetic immunization
Patent: WO 0232943-A 174 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
                                                                                                                               2035 ACAAGAGCGAGAGGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAGGAAAGG
                           AGGAGCCCATCATCGCCCCCGAGACCTTCTACGTGGACGCCGCCCCCAACCGCGAGACCA
                                         2018 AGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCG
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0; Mismatches 178;
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13.21 AGGCCCCCANGCGCCACACAAAGGCCTGCTACAATGCGCCACAGGCAGGC	ACGAGACCCCGGGATCCGCTACCAGTACAACGTGCTGCCCCAGGCTGGAAGGGCAGCCCCAGGACCCCCCGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

542 TGCGCCAGTACGAGATCCTGATCGAGATCTGCGGCAAGGGCCATCGGCACCGTGC 601	662 CCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGAAGCTGAAGCCCGGCATGG 721 [3743 842 3803 902 3863 962 3923	1022 GCGTGCCCCTGGACGACGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACA 1082 ACGAGCCCCTGGACAAGGACTTCCGCAAGTACACCGCTTCACCATCCCCAGCATCAACA 1082 ACGAGACCCCCGGCATCCGCTACAAGGCTGCTGCCCCAGGGCTGGAAGGCCACC 1083 ACGAGACCCCCGGCATCCGCTACAACTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCC 1084 ACGAGACCCCCGGCATCCGCTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCC 1084 ACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCC 1084 ACGAGACCCCCGGCATCCGCTACCAGTACAACGCCCAGGGCTGGAAGGCCAGCCCAGGGCTGCAACACGCCCAGGGCTGCAACACCAGCCCCAGGGCTGCACCCCAGGGCTGCACCCCAGGGCTGCACCCCAGGGCTGCCCCAGGGCTGCACCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGCCCCAGGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGGCTGCCCCAGGCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCCAGGCCCAGCCCCAGGCCCAGCCCCAGGCCCAGGCCCAGCCCCAGGCCCAGCCCCAGGCCCAGGCCCAGCCCCAGGCCCACACCCCAGGCCCAGCCCAGGCCCAGCCCACGCCCAGCCCACACCCACACCCACACCCACACCCACACCCACACCCACA	1142 CCAGCATCTTCCAGGGAGCATGACCAGAGCCCTCCGGGCCCGCAACCCCCCCC	4223 1316 4283 1376 4343	1436 TCCAGAAGCTGGTGACCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTGC 1495
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Qy 2276 CCGCCCACAAGGGCATCGGCGCAACGAGCAAGGTGAAGGTGAAGGCAAGGCAATCC 2335 Db 5235 CCGCCCACAAGGGCATCGGCGGCAACGAGCAGGTGAAGCGCCTGGTGAGCGCCCGCATCC 5294 Qy 2336 GCAAGGTGCTGTTCCTGGACGGCATCGATGGTGATCTACCAGTA 2387 Db 5295 GCAAGGTGCTGTTCCTGGACGGCATCGATGGATGGTATCGTGATCTACCAGTA 2387 Db 5295 GCAAGGTGCTGTTCCTGGACGGCATCGACACAGGAGGAGCACGAGAAA 5346	RESULT 15 Ax427931 LOCUS DEFINITION Sequence 169 from Patent W00232943. ACCESSION AX427931 KEYWORDS SOURCE	NISM Synthetic Other sequ- ORS Huang, Y. e E Modification MAL Patent: WC GOVERNMENT SUCCE I	ORIGIN Query Match B1.4%; Score 2005.2; DB 6; Length 9169; Best Local Similarity 91.4%; Pred. No. 1.4e-200; Matches 2187; Conservative 0; Mismatches 183; Indels 22; Gaps 5; Oy 14 TGGCGAGGCCATGAGCCAGCGCCACACATCTGATGCAGGGCGCAGCACTTCA 73 Db 2967 TGGCCGAGGCCATGAGCCAGCACACACATCATGATGCAGCGGCAACTTCA 3026	Qy 74 AGGGCCCCAAGGGCATCATCAAGTGCTTCAACTGCGGCAAGGGCCACATCGCCCGCA 133 Db 3027 AGGCCCAGAAGCGCATCAAGTGCTTCAACTGCGGCAAGGAGGCCACCTGGCCCGCA 3083 Qy 134 ACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCCACCAGATGA 193 Db 3084 ACTGCCGCGCCCCTGCGAAGAAGGCTGCTGGAAGTGCGCAAGGACGCCACCAGATGA 193 Qy 194 AGGACTGCACCGAAGAAGGCTGCTGCAAGAAGGACCTGCCCCAGGGCA 253 Qy 194 AGGACTGCACCGAAGCCCAAGGCCAACTTCTTCCGCGAGGACTTCCCCCAGGGCA 253	3144 AGGACCGAGCGAGCGAGCTAA-TTTTTAGGAAGATCTGGCCTTCCCACAGGGA 254 AGGCCGGAGTTCCCCAGCGAGCAGAGACGCCAACAGGGA 255 AGGCCGGGAGTTCCTCAGGGAGAGAGACGCCAACAGGGGGGGG	1

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Search completed: June 1, 2005, 20:20:37 Job time: 10550.7 secs

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GARBEAL INFORMATION:

GAPLICANT: BRANETT, Susan

APPLICANT: SRIVASTRAVA, Indresh

APPLICANT: SRIVASTRAVA, Indresh

APPLICANT: LIU, Hong

APPLICANT: LIU, Hong

APPLICANT: SILBY, Mark

CURRENT SILBY

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT APPLICATION VOS: 90

SOFTWARE: PATENTIN VOF: 2.0

SEQ ID NO 84

LIENGTH: 2312
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; OTHER INFORMATION: FS(-).protmod.RTopt(+)
US-09-475-515-84
US-09-117-217-9
US-09-117-217-11
US-09-117-13-13
US-09-135-487-9
US-09-735-487-1
US-09-735-487-1
US-09-735-487-1
US-09-735-487-1
US-09-735-487-1
US-09-706-1487-1
US-09-706-1487-9
US-08-188-848A-9
US-08-188-533-1
US-08-188-533-1
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APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
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APPLICANT: SELBY, Mark
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT PAPLICATION NUMBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
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Pred. No. 0;
0; Mismatches 138; Indels
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; OTHER INFORMATION: FS(-).protmod.RTopt.YM
US-09-475-515-82
BARNETT, Susan
ZUR MEGEDE, Jan
SRIVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.3%;
Matches 2156; Conservative
                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: ZUR NGGEDE, Jan
APPLICANT: LIAN YING
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITILE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
ITILE OF INVENTION: OF VIRUS-LIKE PARTICLES
ITILE OF INVENTION: OF VIRUS-LIKE PARTICLES
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
                                                                  2437
                                                                                                    2209 TCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGCCCCTAGGATCGATT 2268
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TCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGATT
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                                                                                                                                            2438 AAAAGCTTCCCGGGGCTAGCACCGGGGGAATTC
2269 AAAAGCTTCCCGGGGCTAGCACCGGTGAATTC
                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09475515A Patent No. 6602705
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 2158; Conserv
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                       1249 AGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGGCAAGCTGAACTGAACTGGGCCAGCC
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                                                                                     TGCTGCGCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGT
                                                                                                                                                                    1358 GGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCCATCGAGCTGCCCGAGA
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APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 80
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Pred. No. 5.3e-309;
0; Mismatches 235; Indels
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                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.0%;
Matches 2058; Conservative
                                                                                                                                                                                                            LENGTH: 2305
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APPLICANT: STAN MEGEDE, Jan
APPLICANT: STAN STANSTAY, Indresh
APPLICANT: STANSTAYA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Farin
APPLICANT: MILKER, Christopher
APPLICANT: WILKER, Christopher
APPLICANT: WILKER, Christopher
APPLICANT: WILKER, Christopher
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT PELLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 81
LENGTH: 2299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Length 4307;
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Pred. No. 2.8e-278;
0; Mismatches 389; Indels
                                                                                                                                                                                                                                              APPLICANT: Oxford Biomedica (UK) Limited
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 67424-200.
CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 4307
                             2268 AAAAGCTTCCCGGGGCTAGCACCGGTGAATTC
2438 AAAAGCTTCCCGGGGCTAGCACCGGTGAATTC
                                                                                                                                               US-09-552-950-2; Sequence 2, Application US/09552950; Patent No. 6541248; GENERAL INFORMATION:
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Best Local Similarity 82.9%;
Matches 1968; Conservative 0
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                                                                                                                                                                                                                                                              CATCCGCAAGGTGCTGTTCCTGGACGCCATCGA 2369
                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09936572
Patent No. 6783981
GENERAL INFORMATION:
GENERAL INFORMATION:
TILE OF INVENTION: ANTI-VIRAL WECTORS
TILE REFERENCE: 078883/0137
CURRENT APPLICATION NUMBER: US/09/936,572
CURRENT FILING DATE: 2001-12-11
PRIOR PILING DATE: 2000-03-17
PRIOR PLING DATE: 2000-03-17
PRIOR PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENT NUMBER: BEST NUMBER: CONTO NUMBER: CONT
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CGACATACAGAAGCTGGTGGGGAAGTTGAACTGGGCCAGTCAGATTTACCCAGGGATTAA 2604
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                             GACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCA
                                                                   CGGCGTGTACTATGACCCCTCCCAGGACCTGATCGCCGAGAGTCCAGAAGCAGGGGCAAGG
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Patent No. 6783981
GENERAL INFORMATION:
APPLICANT: UDEN, MARK
APPLICANT: MITROPHANOUS, KYRIACOS
TITLE OF INVENTION: ANTI-VIRAL VECTORS
FILE REFERENCE: 078883/0137
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CURRENT APPLICATION NUMBER: US/09/936,572

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Best Local Similarity 82.2%; Pred. No. 1.2e-273;
Matches 1951; Conservative 0; Mismatches 406;
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION WUMBER: PCT/GB00/01002
PRIOR FILING DATE: 2000-03-17
PRIOR PELLING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALENTIN VEY: 2.1
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CURRENT APPLICATION NUMBER: 08/0936,572
CURRENT PAPLICATION NUMBER: 08/09/936,572
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: PCT/GB00/01002
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Pacentin Ver. 2.1
SOFTWARE: 4642
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; Patent No. 6783981
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APPLICANT: MITROPHANOUS, KYRIACOS
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; GENERAL INFORMATION:
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US-09-936-572-12
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                                                                                                                                                                                                                                                                                                                                 Score 1651.4; DB 4; Length
Pred. No. 1.4e-273;
0; Mismatches 406; Indels
                                     2369
                                                  Sequence 5, Application US/09552950
Patent No. 6541248
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 674524_2004
CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DAIE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 5;
                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 82.2%;
Matches 1951; Conservative
                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
US-09-552-950-5
                                                                                               RESULT 12
US-09-552-950-5
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                                                                    Gaps
                                                                    16;
                                 Length 8366;
                                                                  Indels
                                  DB 4;
                                 Score 1592.8; DB 4;
Pred. No. 1.4e-263;
0; Mismatches 442;
                                  64.5%;
80.7%;
                                 Query Match
Best Local Similarity 80.7 Matches 1914; Conservative
 US-09-872-733A-6
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CCAGTGGACCTATCAGATTTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGC 3931
                                                      CCGGATGAGGGGTGCCCACACTAACGACGTCAAGCAGCTGACGAGGCCGTGCAGAAGAT 3991
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                                  CAAGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGAT
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ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
OTHER INFORMATION: of the construct pCMVGagpolBNKan containing a CMV
OTHER INFORMATION: promoter, a HIV gag/pol gene and a kanamycin
OTHER INFORMATION: resistance gene
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Sequence 6, Application US/09872733A

Patent NO. 6656706

GENERAL INFORMATION:
APPLICANT The Government of the United States of America, as
TITLE OF INVENTION: MOLECULAR CLOMES WITH MUTATED HIV GAG/POL, SIV
TITLE OP INVENTION: SIV ENV GENES
TITLE COP INVENTION: SIV ENV GENES
FILE REPERENCE: 2006-4287021 HIV GAG/POL, SIV GAG & ENV
CURRENT APPLICATION NUMBER: US/09/872,733A

CURRENT FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-02
PRIOR PILING DATE: 1999-12-22
PRIOR PILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 19
SOPTWARE: PatentIn Ver: 2.1
SEQ ID NO 600
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                                                                 4076 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGAAAAAGTGTACCTGGCATGGG
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                                                                                                            AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGG
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                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09872733A

Sequence 1, Application US/09872733A

Patent No. 6656706

GENERAL INFORMATION:
TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG

TITLE OF INVENTION: SIV ENV GENES WITH MUTATED HIV GAG/POL, SIV GAG

TITLE OF INVENTION: 120 EV ENV GENES WITH MUTATED HIV GAG/POL, SIV GAG

CURRENT APPLICATION NUMBER: US/09/872,733A

CURRENT APPLICATION NUMBER: US/09/872,733A

PRIOR APPLICATION NUMBER: 60/103,036

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutated Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.1%; Score 1557.4; DB 4; Length 4338; Best Local Similarity 80.5%; Pred. No. 1.5e-257; Matches 1914; Conservative 0; Mismatches 441; Indels 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Mu
OTHER INFORMATION: Immunodeficiency Virus - 1 Gag/Pol gene
                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 1
LENGTH: 4338
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US-09-872-733A-1
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APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.
APPLICANT: Raslow, David C.
APPLICANT: Shiver, John W.
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APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: WACCINES EXPRESSING CODON OPTIMIZED HIVI-GAG, POL, NEF AND
TITLE OF INVENTION: WACCINES EXPRESSING CODON OPTIMIZED HIVI-GAG, POL, NEF AND
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TITLE OF INVENTION NUMBER: US/09/952,060
CURRENT APPLICATION NUMBER: PCT/USO1/28861
PRIOR PRILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-03-07
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2000-09-05
PRIOR FILING DATE: 2000-09-15
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Search completed: June 2, 2005, 03:12:53 Job time: 401.948 secs

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(Ggn2_6/ptodata/1/ina/5A_COMB.seq:*
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      APPLICANT: ZIR MEGEDE, Jan
APPLICANT: ZIR MEGEDE, Jan
APPLICANT: LIAN, YING
APPLICANT: GREER, Catherine
APPLICANT: Mark
APPLICANT: WalkER, Christopher
APPLICANT: WalkER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.00
TITLE OF INVENTION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 84
TENGTH: 2312
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US-09-475-515-84
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 BARNETT, Susan
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RESULT 4

US-09-475-515-6

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JS-09-475-515-6

Sequence 6, Application US/09475515A

Patent No. 6602705

GENERAL INFORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: BARNETT, Susan

APPLICANT: HARTOG, Karin

APPLICANT: WING

TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION

TITLE OF INVENTION: OF VINUE-LIKE PARTICLES

TITLE OF INVENTION: OF VINUE-LIKEN

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2378 TCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGCCCTAGGATCGATTAAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: HIV-Gag-polymerase
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78.9%; Score 1942.6; DB 4;
2al Similarity 89.7%; Pred. No. 0;
2129; Conservative 0; Mismatches 225;
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 2129
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  GCGACCTGGAGATCGGCCACCGCGCCAAGATCGAGAAGCTGCGCAAGCACCTGCTGC
                              1081 GCGACCTGGAGATCGGCCAGCACCACCACCAAGATCGAGGAGCTGCGCCAGCACCTGCTGC
                                                                                                         GCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGG
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                                         780 AGGTGCAGCTGGGCATCCCCCACCCGGCCTGAAGAAGAAGAAGAGGGGTGACCGTGC
                                                                                                                     CCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGC
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                                                                                                                                                                        TGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGG
                                                                                                                                                                                     960 TGCCCCAGGGCTGGAAGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGG
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Pred. No. 7.2e-312;
0; Mismatches 232; Indels
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APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 80
                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.4%;
Matches 2061; Conservative
                                                                                                                   Q ID NO 80
LENGTH: 2305
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.1%; Score 1651.8; DB 4; Length 4307; Best Local Similarity 82.5%; Pred. No. 4.2e-273; Matches 1939; Conservative 0; Mismatches 391; Indels 19;
                                                                                               US-09-552-950-2

Sequence 2, Application US/09552950

Patent No. 6541248

GENERAL INFORMATION:

APPLICANT: Oxford Blomedica (UK) Limited

TITLE OF INVENTION: Anti-Viral Vectors

FILE REFERENCE: 674524-2004-20

CURRENT APPLICATION NUMBER: US/09/552,950

CURRENT FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 2

LENGTH: 4307
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                             SQUENCE 14, Application US/09936572
Patent No. 6783981
GENERAL INFORMATION:
APPLICANT: UDEN, MARK
APPLICANT: UDEN, MARK
APPLICANT: MITROPHANOUS, KYRIACOS
TITLE OF INVENTION: ANTI-VIRAL VECTORS
FILE REPERRACE: 078893/0137
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: PCT/GB00/01002
PRIOR APPLICATION NUMBER: PCT/GB00/01002
PRIOR APPLICATION NUMBER: GB 9906177.2
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PatentIn Ver: 2.1
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ORGANISM: Artificial Seguence
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Matches 1922;
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US-09-936-572-14
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Patent No. 6783991
GENERAL INFORMATION:
APPLICANT: UDEN, MARK
APPLICANT: UDEN, MARK
APPLICANT: MITROPHANOUS, KYRIACOS
TITLE OF INVENTION: ANTI-VIRAL VECTORS
FILE REFERENCE: 078883/0137
CURRENT APPLICATION NUMBER: US/09/936,572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: pSYNGP3-codon
OTHER INFORMATION: optimised HIV-1 gagpol with leader sequence from
OTHER INFORMATION: the major splice donor
                                                                                                                                                                                                                                                                                                                                                                                                Length 4353;
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Pred. No. 1.9e-268;
0; Mismatches 408; I
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/GB00/01002
; PRIOR FILING DATE: 2000-03-17
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4353
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81.8%;
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Best Local Similarity 81.8°
Matches 1922, Conservative
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1218GGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCAGCAGCAGCAGATCGA 1274	1275 GGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCCCGACAAGAAGCACCAGAA 1334	1335 GGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCCCCGACAAGTGGACCGTGCAGCC 1394	1395 CATCGAGCTGCCCGAGAAGGAGAGCTGGAACGACGACACACAGAAGCTGGTGGGCAA 1454	1455 GCTGAACTGGGCCAGCTGTTTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCT 1514 2884 GTTGAACTGGGCCAGTTAACCCAGGATTAAGGTGAGGTG	1515 GCGCGCCCAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCT 1574 [1575 GGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCAA 1634 1004 GGCAGAAAACCGAGAATCCTAAAGGAGCCCGTGCACGGGGTGTACTATGACCCCTCCAA 3063	1635 GGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTACCA 1694 161111	1695 GGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCCACCGCCCACACAA 1754		1815 GGGCAAGACCCCCAAGTTCCGCCTCCCAACGAAGAGCCTGGGAGACCTGGTGGAC 1874	1875 CGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCC	1935 GAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCCAAGACCTTCTACGTGGA 1994		2055 GCAGAAGATCGTGAGCCTGACCGACCACCAGAAGACCGAGCTGCAGGCCATCCA 2114	2115 GCTGGCCCTGCAGACAGCGAGCGAGGTGAACATCGTGACCGACAGCCAGTÀCGCCCT 2174	2175 GGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGCGAGCTGGTGAACCAGATCATCGA 2234	2235 GCAGCTGATCAAGAAGGAAGGTGTACCTGAGCTGGGTGCCCGCCC	2295 CGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGA 2354
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2816 CAACATCATCGGACGCAACCTGTTGACGCAGATCGGTTGCACGCTGAACTTCCCCCATTAG 2875
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                                                   3056 CAAGAAGAACTCCACGAAATGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGGC
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                                      CCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCA
                                                                                      GTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAA
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                                                                                                                                                                                                                                                                                                                                                     Length 9772;
                                                                                                                                                                                                                                                                                                      FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:pSYNGP US-09-552-950-5
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                     Score 1624.6; DB 4;
Pred. No. 2.1e-268;
0; Mismatches 408;
                                                                                                                         Sequence 5, Application US/09552950
Patent No. 6541248
GENERAL INFORMATION:
TITLE OF INVENTION: Anti-viral vectors
FILE REFERENCE: 674524-2004
CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9772
                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%;
Matches 1922; Conservative
                                         2363
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3784 TGGCATCGA 3792
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US-09-552-950-5
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3896 GGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCCGGATGAGGGGTGCCCACACTAA	US-09-872-733A-6
OY 1755 CGACGTGAAGCAGCTGACCGAGGCGGAGAATCGCCATGGAGAGCATCGTGATCTG 1814	4 Query Match 63.6%; Score 1566; DB 4; Length 8366; Best Local Similarity 80.2%; Pred. No. 2e-258; Matches 1885; Conservative 0; Mismatches 446; Indels 19; Gaps 4;
1815 GGGCAAGACCCCCAAGTTCCGCCTCCAGAAGAAGAAGACCTGGGAACCTGGTGGACTTGGTGGACTTCCAGAAGAAGAAGAACCTGGGAACCTGGTGAACTGGTGAACTGGTGAACTGGTGAACTGGTGAACTGGTGAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGGTAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTAACT	Oy 33 GGCCACCAGCGCCAACATCCTGATGCAGCGCAACTTCAAGGGCCCCAAGCGCATCAT
4016 GGGAAAGACTCCTAAGTTCAAGCTGCCCATCCAGAAGGAAACCTGGGAAACCTGGTGGAC	Db 1879 GACGAACTCGGCGACCATAATGATGCAGAGGCAACTTCCGGAACCAGGGAAGATCGT
OY 1875 CGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCC	4 Qy 93 CAAGTGCTTCAACTGCGGCAAGGAGGGCCACTGCGCGCAACTGCCGCGCACTGCCGCAA 152
Qy 1935 GAAGCTGTGGTACCAGCTGGAGAGAGCCCATCATCGCGCCCAGAGACCTTCTACGTGGA 1994 Db 4136 GAAGCTGTGGTACCAGCTGGAGAGGCCCCATAGTGGGCGCCCAAACCTTCTACGTGGA 4195	4 Oy 153 GAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCACCAGATGAAGGACTGCACCGAGCGCCA 212 5 Db 1999 GAAGGCTGTTGGAAATGTGGAAAGGAAGGAACACCAAATGAAAGATTGTACTGAGAGACA 2058
QY 1995 CGGCGCCGAACCGCGAACCAAGATCGGCAAGGCCGGCTACGTGACCGACGGGGCCG 2054	4 Oy 213 GGCCAACTTCTTCGGGAGGACCTGGCCTTCCCCCAGGGCAGGCCGGAGTTCCCCAG 272
OY 2055 GCAGAAGATCGTGACCTGACCGACGACCAGGAGACCGAGGTGCAGGCCATCCA 2114	4 273 CGAGCAGAACCGCGAACAGCCCCACCAGCCGGAGCTGCAGGTGCGCGGGGA 326
OY 2115 GCTGGCCCTGCAGGACAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCT 2174	9 327 CAACCCCGGAGGGGGGGGGCGAGGGCAAGGGCACCCTGAACTTCCCCCA 380 Db 2178 CAACTCCCCCTCAGAAGCAGAGCGATAGAACAGAACTGTATCCTTTAACTTCCCTCA 2237
OY 2175 GGGGATCATCCAGGCCCGACAAGAGCGAGGGGGGGGGGG	9 381 GATCACCCTGTGGCAGCGCCCCCTGGTGAGCTGGGCGGCCAGATCAAGGAGGC 440
OY 2235 GCAGCTGATCAAGAAGAGAAGTGTACCTGAGCTGGGTGCCGCCCCACAAGGGCATGGG 2294	9 441 CCTGCTGGACACCGACGACGACACGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTG 500
QY 2295 CGGCAACGAGCAGTGACCAAGGCATCCGCAAGGTCTGTTCCTGGA 2354 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	9 501 GAAGCCCAAGATGATCGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGAT 560
Qy 2355 CGGCATCGA 2363 Db 4556 TGGCATCGA 4564	Oy 561 CCTGATCGAGATCTGCGGCAAQAAGGCCATCGGCACCGTGCTGATCGGCCCCCCGT 620
RESULT 13 US-09-872-733A-6	0y 621 GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCTGAACTTCCCCATCAG 680
; Sequence 6, Application US/U9872733A ; Patent No. 6656706 ; GENERAL INFORMATION:	681 CCCCATGAGACGGTGAAGCTGAAGCCCGGCATGGACGCCCCAAGGTGAAGAA
	2538
	GIGGCCCLIGACGAGGAGGAGGAGTCAAGGCCCLIGACCCCATIC I GIGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
; PRIOR PELICATION NUMBER: PCT/USO0/34985 ; PRIOR PILING DATE: 2000-12-22 ; PRIOR APPLICATION NUMBER: 60/173,036	QY 801 GGAGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCAT 860
; PRIOR FILING DATE: 1999-12-23 ; NUMBER OF SEQ ID NOS: 19 ; SOFTWARE: Patentin Ver. 2.1	861 CAAGAAGAAGAAGCACCAAGTGGCGCAAGCTGGACTGGA
ì	921 CACCAGGACTTCTGGGAGGTGCAGCTGGGGATCCCCCCCC
ORGANISM: Artificial Sequence PEARINE:	2778 AACTCAGGACTTCTGGGAAGTTCAGCTGGGCATCCCACATCCCGCTGGGTTGAAGAAAAA
CTHER INFORMATION: DESCRIPTION OF ALLITICAL SEQUENCE: CTHER INFORMATION: of the construct pCMVgagpolBNKan containing a CMV CTHER INFORMATION: promoter, a HIV gag/pol gene and a kanamycin CTHER INFORMATION: resistance gene	Qy 981 GAAGAGGTGACCGTGCTGGACGTGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGA 1040

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                                                                         4038 GGGCATCATCCAAGCACAAACCAGACCAATCCGAGTCAGAGCTGGTGAACCAGATCAA
2115 GCTGGCCCTGCAGGACAGCGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCT
               4098 GCAGCTGATCAAGAAAGAGAAAGTGTACCTGGCATGGGTACCAGCACCACAAGGAATTGG
                                                                                                                                                                             2295 CGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGA
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Sequence 1, Application US/09872733A

Patent No. 6656706

GENERAL INFORMATION:

APPLICANT The Government of the United States of America, as

TITLE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV

TITLE OF INVENTION: BIV ENV GENES

FILE REFERENCE: 2026-4287US1 HIV GAG/POL, SIV GAG & ENV

CURRENT APPLICATION NUMBER: US/09/872,733A

CURRENT FILING DATE: 2001-06-01

FRIOR APPLICATION NUMBER: 60/173,036

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 19

NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Mu
OTHER INFORMATION: Immunodeficiency Virus - 1 Gag/Pol gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.1%; Score 1530.6; DB 4; Length Best Local Similarity 80.1%; Pred. No. 2e-252; Matches 1905; Conservative 0; Mismatches 444; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 1
LENGTH: 4338
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US-09-872-733A-1
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APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaalow, David C.
APPLICANT: Kaalow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: WACCINES EXRESSING CODON OPTIMIZED HIVI-GAG, POL, NEF AND TITLE OF INVENTION: WODIFICATIONS
TITLE OF INVENTION: MODIFICATIONS
TITLE OF INVENTION: MODIFICATION NUMBER: POT/USO1/28861
PRIOR FILING DATE: 2001-09-14
PRIOR PILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2001-09-07
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SECTION NO. 1
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ORGANISM: Artificial Sequence
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2601 3 US-09-117-217-9 2601 3 US-09-117-217-11 2601 4 US-09-735-487-7 2601 4 US-09-735-487-7 2601 4 US-09-735-487-11 2601 4 US-09-735-487-13 2601 4 US-09-735-487-13 4307 4 US-09-522-950-1 4307 4 US-09-523-950-1 4307 4 US-09-184-4186-7 7399 2 US-08-148-848A-9 9709 4 US-09-188-8483-5 9709 3 US-08-488-5518-1 9709 3 US-08-488-5518-1 9709 3 US-08-488-5518-1 9709 4 US-09-118-138-138-138-138-138-138-138-138-138	ALIGNMENTS US/09475515A an ndresh togher OVED EXPRESSION OF HIV IRUS-LIKE PARTICLES ER: US/09/475,515A 9-12-30 2.0 quence ription of Artificial).protmod.RTopt.YMWM	# 83.0%; Score 2040; DB 4; Length 2300; imilarity
28 1081.6 44.0 30 1081.6 44.0 31 1081.6 44.0 32 1081.6 44.0 33 1081.6 44.0 34.0 36.0 36.0 36.0 36.0 36.0 36.0 36.0 36	RESULT 1 US-09-475-515-83 Sequence 83, Application US/0947; PAPELONT: BARNETT, Susan APPLICANT: BARNETT, Susan APPLICANT: BARNETT, Susan APPLICANT: LIAN, Ying APPLICANT: LIAN, Ying APPLICANT: LIAN, Xing APPLICANT: LIAN, Xing APPLICANT: LIAN, Xing APPLICANT: GREEK, Catherine APPLICANT: GREEK, Catherine APPLICANT: GREEK, Catherine APPLICANT: GREEK, Catherine APPLICANT: GREEK, CATHERING APPLICANT: BEEK, MALKER, APPLICANT: BEEK, WALKER, APPLICANT: GREEK, CATHERING APPLICANT: SEGO IN ONG YINGS-LII FILE REFERENCE: 1631.002 CURRENT PAING DATE: 1999-12-30 NUMBER OF SEQ ID NOS: 90 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 83 LENGTH: 2300 TYPE: DNA ORGANISM: ATTLIFICIAL SEQUENCE FEATURE: OTHER INFORMATION: PS(-).protm US-09-475-515-83	Query Match Best Local Similarity Matches 2153; Conserv Qy 170 GGGGAAGGA Db 1 GGGGCAGGG Qy 230 AGGACCTGGC Qy 230 AGGACCTGGC Qy 290 ACGCCCCAC Qy 290 ACGCCCCAC Qy 344 CCGGGCCCAC Qy 344 CCGGGCCCAC Qy 346 CCGGGCCCAC Qy 347 CCGGGCCCAC Qy 348 CCGGGCCCAC Qy 340 CCGGGCCCCAC Qy 340 CCGGGCCCCAC Qy 340 CCGGGCCCCAC Qy 340 CCGGGCCCCAC

Page 2

Db 1321 GCATCAAGGTGAAGCTGTGCAAGCTGCGGCGCGCGCACCAAGGCCCTGACCGAGGTGA 1380	QY 1538 TGCCCTGACCGAGGGGGGGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGGGAGC 1597 D 1381 TCCCCCTGACCGAGGAGGCCGAGAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGC 1440	QY 1598 CCGTGCACGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGG 1657 Db 1441 CCGTGCACGAGGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGG 1500	в н	AGTACGCCAAGATGCGCCCACCCAACGACGTGAAGCAGCTGACCGAGGCCGTGC 17	Oy 1778 AGAAGATGGCCATGGAGGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCA 1837	Oy 1838 TCCAGAAGACCTGGAGACCTGGTGGACCGACTACTGGCAGCCACCTGGATCCCCG 1897	AGTGGGAGTTCGTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGTTGGAAAGGAGC 	Qy 1958 CCATCATCGGCGCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGATCG 2017		8 CCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGAGAGAGGGGGAGCGAGG 21 	2138 TGAACATGTGACGACAGCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCAGAGA 21	GCGAGACCAGCTGGTGATCATCATCAGCAGCTGATCAAGAGGAGAAGGTGTACC 	2258 TGAGCTGGGTGCCCCCCCCCACAGGGCATCGGCGGCACGAGCAGTCGACTGGTGA	2118 GCAAGGGATCCGCAAGGTGCTGTTCCTGGACGGCATCGATGGCGGCATCGTGATGCCGCATCGTGATGCCGCATCGTGATGCCGGCATCGGAAGGTGCTGTTCCTGAACGGCATCGATGGCGGCATCGTGATGCCGGCATCGTGATGCCGGCATCGTGATGCCGGCATCGTGATGCCGGCATCGATGCCGGCATCGTGATGCCGGCATCGTGATGCCGGCATCGATGCCGGCATCGATGCCGGCATCGATGCCGGCATCGATGCCGGCATCGATGCCGGCATCGATGCCGGCATCGATGCCGATGCGATGCCGATGCGATGCCGGCATCGATGCCGATGCGATGCCGATGCATGC	2378 AGTACATGGACCACCTGTACGTG	Qy 2438 GGGCTAGCAGGTGAATTC 2457 Db 2281 GGGCTAGCACCGGTGAATTC 2300	RESULT 2 US-09-475-515-82 ; Sequence 82, Application US/09475515A ; Patent No. 6602705 ; GENERAL INFORMATION:
398 GCCCCTGGTGAGCATCAAGGTGGCGGCCAGATCAAGGAGCCCTGCTGGACACCGGCG 457	CCGACGACACCGTGCTGGAGGATGAGCCTGCCCGCAAGTGGAAGCCCAAGATGATCGCCCAAGATGATCGCCCGCAAGTGGAAGCCCAAGATGATCGCCCGCC	GCGGCATCGGCGCCTTCATCATCAGCGCCCGGCCCGGCC	GCGAGGGCGATCGGGGGCGCCCCCCCCCGGGGGGGGGGG	ACATGCTGACCCAGCTGCGCTGCAACTTCCCCATCAGCCCATCGAGACCGTGC	CCGTGAAGCTGAAGCCCGGCATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGG	AGAAGATCAAGGCCCTGACGCCATCTGCGAGGAGATGAAGGAGGGGGAAGATCACCA	818 AGATCGGCCCCGGAGAACCCCCTACAAGACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCA 877	878 CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGG 937	AGGTGCAGCTGGCCATCCCCCCCGCCGCCTGAAAAAAAAA	TGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCG	1058 CCTTCACCATCCCCAGCATCAACAAGACCCCCGGCATCCGCTACCAGTACAACGTGC 1117	1118 TGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGG 1177	AGCCCTTCCGCGCCCGCAACCCCCGAGATCGTGATCTACCAGGCCCCCCTGTACACACAC	1238 GCGACCTGGAGATCGGCCCAGGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGC 1297	1298 GCTGGGGCTTCACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGCCCATCG 1357	1358 AGCTGCACCCCGACAAGTGGACCGTGCAGCGTGCCCCGAGAAGAGAGAG	1418 CCGTGAACGACTCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCA

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                        AGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCA
                                                                                CCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAAGCGCAAGCGCAAGCGCAAGCTTCTGGG
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APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SILVASTAVA, Indresh
APPLICANT: SILVASTAVA, Indresh
APPLICANT: LIJA, YIJA
APPLICANT: LIJA, Walk
APPLICANT: LIJA, HONG
APPLICANT: BELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Catherine
APPLICANT: WALKER, CATHEROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
ITILE OF INVENTION: INPRES: US/09/475,515A
CURRENT PELICAL 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NOS 82
LENGTH: 2306
WUNDER OF SEQ ID NOS: 306
SEQ ID NOS 82
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; OTHER INFORMATION: FS(-).protmod.RTopt.YM
US-09-475-515-82
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| APPLICANT | SURAND |
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| APPLICANT | LIU | HONG |
| APPLICANT | SELBY | Mark |
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| APPLICANT | SURAND | SURBY |
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| APPLICANT | SURAND |
| TITLE OF INVENTION | UMBER: US/09/475,515A |
| CURRENT | APPLICATION | NUMBER: US/09/475,515A |
| CURRENT | SOFT | USS | 90 |
| SOFTWARE | PATENTIN | Ver. 2.0 |
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                                                   AGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCA
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	RESULT 4 US-09-475-515-6 i Sequence 6, Application US/09475515A i Patent No. 6602705 i GENERAL INFORMATION: APPLICANT: BARNET, Susan APPLICANT: SRIVASTAVA, Indresh APPLICANT: LIU, Hong APPLICANT: LIU, Hong APPLICANT: RELBY, Mark APPLICANT: WALKER, Catherine APPLICANT: WALKER, Christopher TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES FILE REFERENCE: 1621.002	NUMBER: US/09/475,515A 1999-12-30 er. 2.0 1 Sequence Description of Artificial Sequence: Bynt	Query Match	
1232 TGGGCAGCGACCTGGAGATCGGCCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACC	1406 AGGAGAGCCGTGAACGACATCCAGAAGCTGGCGCAAGCTGAACTGGGCCAGCC 1465 1261 AGGACAGCTGGAACGACATCCAGAAGCTGGCGCAAGCTGAACTGGGCCAGCC 1320 1261 AGGACAGCTGGAACGACACTCCAGAAGCTGGTGGCGCAAGCTGAACTGGGCCAGCC 1320 1466 AGATCTACCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGGTGCGGCGCCAAGGCC 1320 1321 AGATCTACCCGGCATCAAGGTGAACGCTGTGCAAGCTGCTGCGGGGCACAGGCC 1380 1526 TGACCGACATCGTGCCCCTGACCGAGGAGCCCGAGGCCC 1380 1527 TGACCGACATCGTGCCCCTGACCGAGGAGCCCGAGGACCTGGCCGAGAACCCCCGAGGCC 1380 1586 TCCTGCGAGGTCACTGACCGAGGAGCCCAGGCTGGAGCTGGCCGAGAACGACCGGAGA 1440 1586 TCCTGCGCGAGCCCTGACCGAGGAGCCCAAGACCTGGTGGCCCGAGA 1500 1641 TCCTGAAGGAGCCCGTGCACGAGGTGGACCCCAAGGACCTGGTGGCCGAGA 1500 1646 TCCTGCAAAGCAGGCCAACGACGAGCTACCAAGAACCTGGTGGCCGAGA 1500		1881 TCARGCTGCCCAGAAGGAGACCTGGGAGGCCTGGTGGAGGAGGCCA 1740 1886 CCTGGATCCCCGAGTGGAGATTCGTGAACACCCCCCCCTGGTGAAGCTGTGGCAGGCCA 1740 1741 CCTGGATCCCCGAGTGGAGATTCGTGAACACCCCCCCTGGTGAAGCTGTGGTACCAGC 1800 1946 TGGAGAAGGAGCCATCATCGGCGCCAGAACCTTCTACGTGAAGCTGTGGACGCCCGC 2005 1801 TGGAGAAGGAGCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCCACCGCG 2005 2006 AGACCAAGATCGGCCATCGTGGGCGCCCAGAGCTGCGTGACGCCCCAACCGCG 1860 2006 AGACCAAGATCGGCGACACGCGGCGCCGAGAGCTACGTGAACGTGTGAGCC 2065 1861 AGACCAAGATCGGCGACTACGTGACCCACCGGGGCCCGAGAAGATGGTGAGCC 1850	

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APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 91
LENGTH: 2299
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                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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                    GCAAGGCCGGCTACGTGACCGACCGGCCGGCAGAAGGTGGTGGTGGTGGTCGCCGACACCA
                                                          CCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGCCAGCGAGG
                                                                                   TGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGA
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; OTHER INFORMATION: FS(+).proinact.RTopt.YM
US-09-475-515-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.4%; Score 1852; DB 4; 3
Best Local Similarity 89.0%; Pred. No. 7.5e-307;
Matches 2052; Conservative 0; Mismatches 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/09475515A
Patent No. 6602705
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: SIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIJU, Hong
APPLICANT: LIJU, Hong
APPLICANT: LIJU, Hong
APPLICANT: LIJU, Hong
APPLICANT: GENEY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: GREEK, Catherine
APPLICANT: GREEK, CATHEROWED EXPRESSION OF HIV POLY
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: SOFTWARE: PATENTING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 80
LENGTH: 2305
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                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence:gagpol-SYNgp - codon CTHER INFORMATION: optimised gagpol sequence US-09-552-950-2
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                                                                                                          Sequence 2, Application US/09552950
Patent No. 6541248
GENERAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 674524-2004
CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIN Ver. 2.1
SSEQ ID NO 2
LENGTH: 4307
2457
                 2280 TTCCCGGGGCTAGCACCGGTGAATTC 2305
2432 TTCCCGGGGCTAGCACCGGTGAATTC
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-552-950-2
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          CCGTGCAGAAGATCGCCATGGAGATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCC 1831
                                                                                              AGGAGCCCGTGCACGAGGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGA 1499
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9 US-09-936-572-14

i Sequence 14, Application US/09936572

i Patent No. 6783381

i GENERAL INFORMATION:

APPLICANT: UDEN, WARK

APPLICANT: WITTOPHANOUS, KYRIACOS

I TITLE OF INVENTION: ANTI-VIRAL VECTORS

FILE REFERENCE: 078883/0137

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US/09/936,572

CURRENT FILING DATE: 2000-03-17

PRIOR FILING DATE: 1999-03-17

PRIOR FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 14

LENGTH: 4327

TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence: PEATURE:

COTHER INFORMATION: sequence of HIV-1 gagpol with 20bp of the leader US-09-936-572-14
                                                        CGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTGCTGACTTGAGCTGTGATCATCAGCAGCTGATCAACGAGCTGATCAAGAAGGAAAGGAAAGGTCTATCTGGCCTG
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                          1106 cergeereaegeceargageceaegreaeceaecracearcareargeaegegeaa
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     CGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGAGCCACAAGAGCGAGAG
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Pred. No. 9e-264;
0; Mismatches 411; Indels
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                                                                                                                                                                                       CATCAGGAAGGTGCTATTCCTGGATGGCATCGA 3457
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Best Local Similarity 81.5%;
Matches 1934; Conservative 0
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FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: pSYNGP3-codon
OTHER INFORMATION: optimised HIV-1 gagpol with leader sequence from
CTHER INFORMATION: the major splice donor
US-09-936-572-13
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: PCT/GB00/01002
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: GB 9906177.2
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 73
; SOSTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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  CGACATACAGAAGCTGGTGGGGAAGTTGAACTGGGCCAGTCAGATTTACCCAGGGATTAA 2604
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                                   GACCGAGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTGCGCGCGAGCCCGTGCA
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                                                                                   CCTGGCTGAGGCCATGAGCCAGGTGACCCAACTCCGCTACCATCATGATGCAGCGCGGGAA
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                                                                CTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGC
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                                  Gaps
                                  28;
 Length 4353;
Score 1599.4; DB 4; Length
Pred. No. 9e-264;
0; Mismatches 411; Indels
Query Match 65.1%;
Best Local Similarity 81.5%;
Matches 1934; Conservative 0
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Sequence 13, Application US/09936572
Patent No. 6783991
GEBERAL INFORMATION:
APPLICANT: UDEN, MARK
APPLICANT: MITROPHANOUS, KYRIACOS
TITLE OF INVENTION: ANTI-VIRAL VECTORS
FILE REFERENCE: 078883/0137
CURRENT APPLICATION NUMBER: US/09/936,572

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GGNAACCTGGGAAACCTGGTGGACAGAGTATTGGCAGGCCACCTGGATTCCTGAGTGGA
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                                          GTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCAT
                                                                       CGGCGCCGAGACCTTCTACGTGGACGCCCCCCCAACCCGCGAGACCAAGATCGGCAAGGC
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Best Local Similarity 81.5%; Pred. No. 9.1e-264;
Matches 1934; Conservative 0; Mismatches 411; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCCGCAAGGTGCTGTTCCTGGACGGCATCGA 2357
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Patent No. 6783901

GENERAL INFORMATION:
APPLICANT: UDEN, MARK

APPLICANT: UDEN, MARK

TITLE OF INVENTION: ANTI-VIRAL VECTORS
FILE REFERENCE: 07883/0137

CURRENT APPLICATION NUMBER: US/09/936,572

CURRENT FILING DATE: 2001-12-11

PRIOR APPLICATION NUMBER: PCT/GE00/01002

PRIOR APPLICATION NUMBER: GB 9906177.2

PRIOR FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 12

LENGTHARE: PATENTIN VET. 2.1

SEQ ID NO 12
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                   2031 GGACTTCCGCGAGCTGAACAAGCGCACGCAAGACTTCTGGGAGGTTCAGCTGGGCATCCC
                                                                                                                                                                                     CTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCAT
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  CGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCC
                                                          CTACAACACCCCCCGTGTTCGCCATCAAGAAGAAGACAGCAGCACCAAGTGGCGCAAGCTGGT
                                                                                                                  GGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCC
                                                                                                                                                                        CCACCCCCCCCCCGCCTGAAGAAGAAGAAGAGCGTGACGTGCTGGACGTGGCGCGACGCCTA
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Pred. No. 1e-263;
0; Mismatches 411;
                                      CATCCGCAAGGTGCTGTTCCTGGACGGCATCGA 2357
                                                                                                                          Sequence 5, Application US/09552950
Patent No. 6541248
GENERAL INFORMATION:
TITLE OF INVENTION: Anti-Viral Vectors
FILE REFERENCE: 674524-2004
CURRENT APPLICATION NUMBER: US/09/552,950
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5:
LENGTH: 9772
                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 81.5%;
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US-09-552-950-5
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                                CCGGATGAGGGGTGCCCACACTAACGACGTCAAGCAGCTGACCGAGGCCGTGCAGAAGAT
                                                                                                                                                  GTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTCGAGAAGAAGAAGCCCATCAT
                     CAAGATGCGCACCCCCACACCACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGAT
                                                               CGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAA
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                                                                                                                      CGGCGCGAGACCTTCTACGTGGACGCCGCCGACCGCGAGACCAAGATCGGCAAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         partent No. 6656706
| Batent No. 6656706
| GENERAL INFORMATION:
| APPLICANT: The Government of the United States of America, as APPLICANT: The Government of the United States of America, as ITILE OF INVENTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV ITILE OF INVENTION: SIV ENV GENES
| TITLE OF INVENTION: SIV ENV GENES | FILE REPRENCE: 2026-4287051 HIV GAG/POL, SIV GAG & ENV CURRENT APPLICATION NUMBER: US/09/872,733A | CURRENT FILING DATE: 2000-0-0.
| PRIOR APPLICATION NUMBER: PCT/US00/34985 | PRIOR PLILING DATE: 1999-12-23 | PRIOR FILING DATE: 1999-12-23 | NUMBER OF SEQ ID NOS: 19 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NOS: 19 | SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCAGGAAGGTGCTATTCCTGGATGGCATCGA 4564
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-872-733A-6
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                                                                  Gaps
                                                             28;
                     Length 8366;
              Score 1539.2; DB 4; Length
Pred. No. 1.8e-253;
); Mismatches 448; Indels
62,6%; Sured
79,9%; Pred
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TACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGGA 4195
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AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCGGCGGGGGGAGGTGAACATCG
                         AGACTGGAGCTGCAAGCCATCTACCTAGCTCTGCAAGACAGCGGACTGGAAGTGAACATCG
                                                                                                    4076 AGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGAGAAAGTGTACCTGGCATGGG
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                                                                                 TGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated Human
OTHER INFORMATION: Immunodeficiency Virus - 1 Gag/Fol gene
US-09-872-733A-1
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| Sequence 1, Application US/09872733A
| Patent No. 6656706
| GENERAL INPORMATION
| TITLE NOT INVERTION: MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV |
| TITLE OF INVENTION: SIV ENV GENES
| TITLE OF INVENTION: SIV ENV GENES
| FILE REFERENCE: 2026-4287US1 HIV GAG/POL,SIV GAG & ENV |
| CURRENT APPLICATION NUMBER: US/09/872,733A |
| PRIOR FILING DATE: 2001-06-01 |
| PRIOR FILING DATE: 2001-22 |
| PRIOR PILING DATE: 1999-12-22 |
| PRIOR PELING DATE: 1999-12-23 |
| NUMBER OF SEQ ID NOS: 19 |
| SEQ ID NO |
| SED ID NO |
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Best Local Similarity 79.8
Matches 1896; Conservative
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                                                                                                                                                         POL,
APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Shiver, John W.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: ENHANCES EXPRESSING CODON OPTIMIZED HIVI-GAG, POL,
TITLE OF INVENTION: WOLFICATIONS
FILE OF INVENTION: WOLFICATIONS
FILE OF INVENTION: WOLFER EXPRESSING CODON OPTIMIZED HIVI-GAG, POL,
TITLE OF INVENTION: WOMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
FRIOR APPLICATION NUMBER: PCT/US01/28861
FRIOR PILING DATE: 2001-09-14
FRIOR PILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-14
FRIOR FILING DATE: 2001-09-15
FRIOR FILING DATE: 2001-09-15
FRIOR FILING DATE: 2001-03-3,180
FRIOR FILING DATE: 2001-03-15
FRIOR FILING DATE: 2000-09-15
FRIOR FILING DATE: 2000-09-15
FRIOR FILING DATE: 2001-03-16
FRIOR APPLICATION NUMBER: 60/233,180
FRIOR FILING DATE: 2001-03-15
FRIOR FILING DATE: 2000-09-15
FRIOR F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Codon optimized DNA encoding modified wt pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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2340 GTTCCTGGACGGCATCGA 2357 1695 GTTCCTGGATGGCATTGA 1712 දි දි

Search completed: June 2, 2005, 03:13:16 Job time: 399.052 secs

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rockefell

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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/organism="Zea mays"
/organism="Zea mays"
/mol type="qenomic DNA"
/etain="W22 (ACR, bz1-m9)"
/cultivar="Uniformulu"
/db_xref="teaxon:4577"
/clone="loss049-08A1-C03"
/clone=lib="UniformNu MUTAIL Library"
/clone lib="UniformNu MUTAIL Library"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformNu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; PACCAD clade, Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 330)
Lateshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
                                                                                                                                                                                                     Tetraodon
OGWCO51TH
OBIFCC026
                                                                                                                                                                                                                                                               BNEL24e3
HVSMEh009
OSJNEb12C
OSJNEb16L
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rockefell
170006873
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CL293849-08A1-CO3 UniformMu MuTAIL Library Zea mays genomic clone 02S0349-08A1-CO3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence flanking probable Mu insertion site in UniformMu line: 0280349-08, Primer set: A Class: transposon insertion site. Location/Qualifiers
B1724851
BM321023
BM321023
CL982362
CL972679
CR603312
AY401196
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Plant Molecular and Cellular Biology Program
University of Florida
1010690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufl.edu
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                                                                                                                                                                                                                                                                                    BE601575
CB648640
CB651670
CB642928
CB641397
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CR603312
AY401196
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CB643171
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CG260623
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Best Local Similarity
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KEYWORDS
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AY103647 2ca mays
CL973991 OBIFCC025
CL961989 OBIFCC025
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CL971508 OBIFCC021
CK159167 FGAS04056
BM320864 rockefell
CM92090 rockefell
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CL974989 OBIFCC031
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CL97091 OBIFCC025
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CL95225 OBIFCC017
CL95225 OBIFCC002
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CL952031 OBIFCC017
BM321022 rockefell
CL9522701 OBIFCC017
CL952271 OBIFCC017
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                   GenCore version (c) 1993 - 2005
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9b_htc::
9b_htc::
9b_est4::
9b_est5::
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9b_gs81::
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Score

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Result

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CGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGT 1025
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                             ceacrescaggactrogregocardercerectectedrearcactecacardatra
                                                                                                    CAACATCGGCCACTTCCAGCTCGTGCTCACGGCCATCGGCAACTTCTGCATCATCTCCAT 758
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GGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCCACCAGCCGCGGA
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                                                                   GCTGCAGGTGCGC---GGCGACAACCCCCGCAGCGAGGCCGCCGAGGCGCCAAGGGCAC
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OBIFCCO15718 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL967755.1 GI:52390149
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae, Oryza.

1 (bases 1 to 2886)
Ma,L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Wong, G.K.S., Deng,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Mong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and Lits comparison to Arabidopsis
Unpublished (2004)
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42.8%; Pred. No. 9.6e-08;
iive 0; Mismatches 915; Indels
Indels
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Tel: 86-10-80481559
Fax: 86-10-80488676
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Mismatches 106;
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/mol_type="Genomic DNA"
/db_xref="taxon:19946"
/clone lib="Oryza sativa E:
/note="Oryza sativa E:
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Rice genomic sequence.
Class: exon-trapped.
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 62211, USA
Missouri, Columbia, MO 6211, USA
Missouri, Columbia, MO 6211, USA
Missouri, Columbia, MO 621, WW. CMD 8010 as tate.edu, TIGR,
WWW.tigr.org; or NUBI, WWW.ncbi.nlm.nih.gov. When the source of the
maize CDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
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                                                           GAAGAGCAAGGAGCGAGCCGAGCCATGGCAGTTCGTCGCCTCCTGCCGCTGTTCGA
                                                                                           CAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCT
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Spermatophyta, Magnolliophyta, Lillopsida, Poales, Poaceae,
Clade, Panicoideae, Andropogoneae, Zea.

    (bases 1 to 2598)

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/db_xref="MaizeDB:638378"
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/note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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Oryza sativa (indica cultivar-group)

SM Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryz
                                                          3069 bp DNA linear GSS 21-SEP-2004 OSIFCC025416 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. CL973991. GI:52402507
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1 (bases 1 to 1398)
Ma.L., Wang,X., Ren,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,M., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Mong,G.K.S., Deng,X.W. and Wang,J.
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Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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Rice genomic sequence.
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Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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/clone_lib="Mastigamoeba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .039 ATCTACGACCCCCAGGTGACGGAGGACCAGGTCCAGCGGGGGACCTCGCCATGAGCAAGTTC 1098
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           514 GCCGTCCAGGCGCTCAAGGACGTGTACGCCCGATGGGTCCCCCGAGGAGGATC---CTC
                                                                                  GCCGCCCAGATCAAGGAGGCCCTGCTGGACACCGGCGGCCGACGACGACGTGCTGGAGGAG
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Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
                                                                                                                                                             Accaccaaccretegrececesegererecaagereseceseseaceserrecreseceas
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Mastigamoeba balamuthi
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BM321451.1 GI:18055857
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OUNTED SEATIVE (indice cultiver-group)

OUYZE SEATIVE (indice cultiver-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartcoideae; OuyZeae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCAGCAACTICAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACGGCGCCAACAGCCCCACC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 GAGGCCTÁCCTCGGCTCGTCCATCAAGAACGCCGTGGTCÁCCGTCCGGGCCTACTTCAAC 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACTCGCAGAGGCCACCAAGGACGCCGGCGTCATCGCCGGGCTCAACGTGATGCGC 522
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                                                                                                                                                  Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (indica cultivar-group)"
/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic By46"
/clone lb="foryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%; Score 84.2; DB 9; Length 1941; Best Local Similarity 42.5%; Pred. No. 6.3e-05; Matches 705; Conservative 0; Mismatches 933; Indels 21
cultivar-group) genomic, genomic survey sequence.
CL971508
CL971508.1 GI:52397596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: chenchen@genomics.org.cn
Rice genomic sequence.
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1. .1941
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AAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAG---AAGGCCATCGGC
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BM320864 linear EST 03-JAN-2002 rockefeller.0.46 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mastigamoeba balamuthi"
/mol type="mRNA"
/mol xrain="ATCC 30984"
/db xref="taxon:10867"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
                    The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002) 21819461
                                                                                                                     <u> AAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAG</u>
                                                                                                                                                                                                                                                                          940 GTGCAGCTGGGCATCCCCCACCCGCCGCCTGAAGAAGAAGAAGAAGAGCGTGACCGTGCTG
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1132)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W., Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and Philippe,H.
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The Rockefeller University
1230 York Avenue, New York, NY 10021, USA
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1132 Std Error: 0.00
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1C101 Engineering Building, 57 Campus Drive, Saskatchewan, S7N 5A9, Canada
Saskatchewan, 37N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phras equence is the direct result of the Base calling software
Cdefault parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,636].
Plate: Tail537 row: N column: 23.
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/wollivar="Minat line PI 178383"
/wollivar="Minat line PI 178383"
/db xref="Laxon:455"
/lab host="DHS alpha"
/clone lib="Triticum aestivum FGAS: Talt5"
/note="Organ: Crown; Vector: pGBM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days (equal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart
                                                                                                                                                                         CK159167 185-2003 869 bp mRNA linear EST 05-DEC-2003 PGAS040564 Triticum aestivum FGAS: Talt5 Triticum aestivum cDNA,
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                                                                                                                                                                                                                                                                                                                         Triticum aestivum (bread wheat)
Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Junes, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F. Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGTGAACATCATCGGCCGCAAC
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Pred. No. 0.00027;
0; Mismatches 374; Indels
                          1780 GCCGACGAGTTCGAGGACAAGATGAAGGAGCTGGAGGGC 1818
1603 CACGCCGTGTACTACGACCCCAGCAAGGACCTGGTGGCC 1641
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CK159167.1 GI:38985053
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Best Local Similarity 44.9%;
Matches 305; Conservative
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba
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                                                                                                                                                        CGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTG 318
                                                                                                                                                                                                       319 CGCGGCGACAACCCCCGCAGCGAGGCCGGCGCCGAGGCCCCAGGGCACCTGAACTTCCCC 378
                                                                                                                                                                                                                               GAGCTCACCCGCTTCGGCGTCAAGCTCGGCCTGACCAACTACGCCGCCGCCTACGCGACT 312
                                                                                                                                                                                                                                                       CAGATCACCCTGTGGCGCCCCCCTGGTGAGCATCAAGGTGGGCGCCCAGATCAAGGAG 438
                                                                                                                                                                                                                                                                              GCCTGCTGCTGCCCGCCGTGTGCTGAAGAAGCTCAACCTCGACTCCAAGTACGAGGGT 372
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                                                                                                                               Tacaacaccccaactaccccritccic----crccccrrcaccaacagesacarcitc
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                                                                                                       TGCACCGAGCGCCAGCCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCCAGGGCAAGGCC
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                                  Gaps
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           Length 1132;
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        Score 80.2; DB 4; Length 1 Pred. No. 0.00032; 0; Mismatches 444; Indels
          3.3%;
                                 Conservative
        Query Match
Best Local Similarity
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BM320900 1165 bp mRNA linear EST 03-JAN-2002 rockefeller.0.353 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA

LOCUS DEFINITION BM320900

GI:18055306

BM320900.1

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Mastigamoeba balamuthi Mastigamoeba balamuthi

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/mol_type="mRNA"
fwol_type="mRNA"
strain="ATCC 30984"
/db_xref="taxon:10860"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                                                                                                                                                     The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002) 21819461
1 (bases 1 to 1165)
Bapteste, B., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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45.1%; Pred. No. 0.00041;
ative 0; Mismatches 506; Indels 16;
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Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1165 Std Error: 0.00
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OBIFCC031917 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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                                                                                                                                                                      AACTCGACGAGGCCAAGTTCAAGCTCGGCAAGGTCCGCCGCGTGCAGCTCGGCAACAAG 430
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
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Bernartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
1 (bases I to 1725)
Ma.L., Wangc, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and Unpublished (2004)
                              GCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGAACCGCGCCAACAGCCCC
                                                                         311 ACCGACGAGCACTTCCGCCTGCTCTACGACACCAAGGGCCGCTTCCAGGCGCACCGCATC
                                                                                                                                                                                                                         CGCCAGGGCACCCTGAACTTCCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATC
                                                                                                                                                                                                                                                                                                                                                                    491 AAGGTCAACGACACGGTCAAGATCGACCTGCGCCTCGGGCAAGATCATCGACTTCGTCAGG
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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Mol Lype="genomic DNA"
/db xref="taxon:39946"
/clone_lib="Oryza sativa Express Library"
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/mol_type="mRNA"
/strain="AATCC 30984"
/db_xrain="AATCC 108607"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                 ceschachicercacceaececcaccecacceeraceaecenacereaeceraea
                                                                                                                                                                 CCTGCGCGAGCCCGTGCTACGTGTACGACCCCAGCAAG---GACCTGGTGGCCGA
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
I (bases 1 to 867)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W., Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and Philippe,H.
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The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 867 Std Error: 0.00
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ilarity 43.5%;
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2031 bp DNA linear GSS 21-SEP-2004 OSIFCC042895 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
1036 GACCGGGAGCCCACGGAGATTGCCGCCATGATCGAGCAGGAGATCGTGAGGTTGGTACCA 1095
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 2031)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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/db_xref="taxon:39946"
/clone_lib="Oryza sativa
/note="Oryza sativa
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Bukaryota, Wagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaa.
I bases 1 to 2697)
Ma,L., Wangc,J., Chen,C., Liu,K., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
Manalysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                       2223 CATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCCCCCACAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2283 CATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTT
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
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Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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GGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCC 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCATCCGCTACCAGTACAACG-----TGCTGCCCCAGGGCTGGAAGGGCCAGCCCCAG
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                                                                                                                   645 CAACGAGCCCACCGCCGCCGCCATCGCCTACGGCATCGACAAGAAGGACGCCGAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGCCCCATCGAGCTGCCCGAGAAGGAGGCTGGACCGTGAACGACGACAGAAGCTGGT
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373 TICCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATC 4	CAGATC 432
433 AAGGAGGCCTGCTGGACACCGGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCC 4	CTGCCC 492 STGGCG 1440
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673 CCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCGGCATGGACGCCCCAAG 7	CCCAAG 732 ITCGGC 1674
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913 AACAAGGGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGGCCGG	3GCCTG 972 3GCAAG 1911
973 AAGAAGAAGAAGGTGACGTGGTGGACGTGGGGGGACGCCTACTTCAGCGTGCCCTG 1	ccccrg 1032 CTCc 1969
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1213 TACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACGGCCCAAGATC 1	AAGATC 1272 ACTCC 2202
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1393 GAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTG 1	AAGCTG 1452

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OBIFSB005 OBIFCC035

OsIFSB004

OSJNED03F OSJNED01A OSJNED16H

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CL982770 CL948321 BM32048331 CL948533 CL947314 CL977314 CC673312 BM321393 CL972100 CC675888 CC675888

BNEL24e3

Title: Perfect score:

Sequence:

nucleic

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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/organism="Zea mays"
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/eultivar="Uniformulu"
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/elon="10:203149-08A1-033"
/elon="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
Uniformulu maize population by the thermo assymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."
                                                                                                                                                                                                                                                                                                                                         linear GSS 12-FEB-2004
Zea mays genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.

1 (Dass 1 to 330)
Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence flanking probable Mu insertion site in UniformMu line: 0280349-08, Primer set: A Class: transposon insertion site. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 136.4; DB 9; Length 330; 66.4%; Pred. No. 2.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
1010690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drm@ufl.edu
                                                                                                                                                                                                                                                                                                                                         330 bp DNA 0250349-08A1-C03 UniformMu MuTAIL Library 02S0349-08A1-C03, genomic survey sequence.
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
Searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t
maize CDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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Clade; Panicoideae; Andropogoneae; Zea.
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shrhartoideae; Oryzae; Oryza CL961989 1398 bp DNA linear GSS 21-SEP-2004 OSIFCCO06991 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence. 'n 225 120 180 CGGATGATCGCCCCGTGGCGACGTCCGACAGGTCGTCGTCGAGAAGTCCACCGTGCCG 342 240 drcaagaccecegadeccarcaagaadarccrcaacacacacaccececacacacarcaec TTCCCCCAGGCCAAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACC 300 462 AGCCGCGAGCTGCAGGTGCGCGGCGACCCCCGCAGCGAGGCCGGCGCGCGGCGAAGGCCAAG 360 420 480 9 GCCGTCCAGGCGCTCTAAGGACGTGTACGCCCCGATGGGTCCCCCGAGGAGGATC---CTC CACATCGCCCGCAACTGCCGCGCCCCCCCGCAAGAGGGCTGCTGGAAGTGCGGCAAGGAG GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCC GGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCCCCCCTGGTGAGCATCAAGGTG GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCCAACATCCTGATGCAG <u>ercadasecacercecedadecesacarecrererereceradadacaceceacade</u> CGCAGCAACTTCAAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGC GGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAG rriccagancenerceaaeeegaagiricenegegaagagagaeegegaeeeneegaaeene /organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
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                                              ATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGATCGGCGGCCATCGGCGGCTTCATCAAG
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (bases 1 to 951)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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Chinese Academy of Sciences, Beijing 101300,
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	RESULT 7 CL978463 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS CL978463 LOCUS CL978463 LOCUS CL978463 CL978463	REFERENCE 1 (bases 1 to 1725) AUTHORS Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jaco,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,Y., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J. TITLE An analysis of transcriptional regulation of the rice genome and tes comparison to Arabidopsis JOURNAL Unpublished (2004) CONMENT Department of Bioinformatic Bejing Institute of Genomics Chinese Academy of Sciences, Bejing 101300, China Tel: 86-10-804881559 Fax: 86-10-804881559 Fax: 86-10-804881559 Fax: 86-10-804881659 Fax: 86-10-804881659	Rice genomic sequence. Class: exon-trapped. 11725 source	Qy 949 GGCATCCCCACCCGGCCTGAAGAAGAAGAAGAAGACGTGACCGTGCTGGACGTGGGC 1008 Db 76 GTCCTCCGCACCCCGGCTGTACGCGGAGGTGACCTCTCGCCGAC 135 Qy 1009 GACGCTACTTCAGCGTGCCTGCCTGCGATGTACGCGGAGTCACCTCTCGCCACCTCTCGCCGCCTCCTCGCCTCCTCGCCTCCTCCGCCTCCT

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       1522 AAGCTGGTCCGGCTGTGGGTCGCCGAGGGTTCATGCAGGCGAAGAACGGGCAGACGGTG 1581
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Enkaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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Pooideae; Triticeae; Triticum.
1 (bases 1 to 869)
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                                                 Contact: Chen Chen
Department of Bicinformatic
Beljing Institute of Genomics
Chinese Academy of Sciences, Beljing 101300, China
Tel: 86-10-8048855
Fax: 86-10-8048856
Email: chenchendegenomics.org.cn
Rice genomic sequence.
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An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                                                           CCCCAGGGCTGGAAGGCCAGCCAGCATCTTCCAGAGCATGACCAAGATCCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OSIFCC021485 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol type="genomic DNA"
/clone llb="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic sequences
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Trache
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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Pred. No. 0.00026;
0; Mismatches 1004; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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ilarity 42.4%;
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Contact: Chen Chen
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Matches 757; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,63].
Plate: Tale537 row: N column: 23.
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Allard, F., Crosby, W.L., Danyluk, J., Budes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, B.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Punctional Genomics of Abiotic Stress In Wheat and Canola Crops
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/lab host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS: TaLt5"
/clone_lib="Triticum aestivum FGAS: TaLt5"
/note="Organ crown; Vector: pGEM-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 21 days and 49 days p178383 cold hardened at 2 C for 21 days and 49 days cequal amount of cDNA pooled together before subtraction, tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (driver). Modified Smart cDNA (Clontech) priming and non-directional cloning"
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                                                                                                                                                                                                                                                                                          Department of Computer Scie 57 Campus Drive, Saskatoon,
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/cultivar="Wheat line PI 178383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Triticum aestivum"
                                                                                                                                                                                                                                                     Bioinformatics
University of Saskatchewan, Departion Engineering Building, 57 (Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769
Fax: 306 966 2033
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                                                                                                                                                                                  Unpublished (2003)
Contact: Wm L Crosby
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Best Local S:
Matches 305
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BM320864 linear EST 03-JAN-2002 rockefeller.0.46 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
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                           GCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCCGTGCACGGCGTGTACTACGACCCCAG 1631
                                                                                                                                                                                                                                                                   CTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTG 1871
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                                                                                                                                                                                                        1539 GCGGCTGAGCAAGGAGGAGATCGAGAAGATGGTGCAGGAGGCGGAGAAGTACAAGGCCGA
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                                                                                                                                                CAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTA
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Muller, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The analysis of 100 genes supports the grouping of three highi
divergent amoebae: Dictyostelium, Bntamoeba, and Mastigamoeba
Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
21819461
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1 (bases 1 to 1132)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, Philippe, H.
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balamuthi"
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The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmullerorockvax.rockefeller.edu
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/clone lib="Mastigamoeba
/note="syn: Phreatamoeba
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rne analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)

USA

Contact: Muller Miklos
Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.

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329 279 449 399 509

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BM320900.1 GI:18055306

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE

вефиепсе. BM320900

LOCUS DEFINITION

BM320900

THE GOOD CONTRICTION OF THE PROPERTY OF THE PR	3111 ACTGGCGGTGGACAAGCTCCATCGGCCGCGCGTGCCCAACACCATCGGCCTCAA 3170 330 CCCCCGCAGGAGCCGAGGCCCAGGGCACCCTGAACTTCCCCCAGGTCACCCT 389 1171 CCCCGAAGCCGTGAGGCTCGAGGCGCGGCCATCGTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGCTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGGTCACTGTCACTGGTCACTGTTCATCACTGGTCACTGGTCACTGTTCATCACTGTTCACTGGTCACTGGTCATTCACTGGTCATTCAT	3411 CCGCACCAGCAGCACCAGCGACGCGACACACAGGCCGGCACCTTCCCGTT 3470 624 CATCATCGGCGCACACAGCCGGCGGCGCGCACCTTCCCGTT 3470 624 CATCATCGGCGCACACACGCGGCGCGCGCACCCTCCGTCAGCCC 683 1471 CCTGGCGAACGGCGCCCGTGAGCTGGACGCCCGACGCACGC		1152 CCAGAGCAGGACGCAGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGAT
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671 GGCCACCAGTTCGCGACGCGCCTGACCAACGTCTTCGTGATCGGCAAGGGCACCAAGTCC 730
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrattoideae; Oryzaee; Oryza.
I Cases I to 2682)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wang,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                        595 ACCGTGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCCAGCTG 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    731 CTCGTCACGCTGCCCGCCGCCAAGGGCCATCAAGAAGTCGATCATCGAGGAGTTCCAGGCG 790
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611 ATTGTGCGCCGCGAGAGCACGAGGGCTCGTTCGAGATCATCCACGTCAAGGACGCCGTC
                                                                          415 AAGGTGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTG
                                                                                                                        491 AAGGTCAACGACACGGTCAAGATCGACCTGCGCCTCGGGCAAGATCATCGACTTCGTCAGG
                                                                                                                                                                      GAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCCAAGATGGATCGGCGGCATCGGCGGCTTC
                                                                                                                                                                                                                      551 TTCGAGATCGGCAACCTCGTCATGATCACTGGCGGACGCAACCTTGGCCGCGTCGGCGTC
                                                                                                                                                                                                                                                                       535 ATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGAGGCCATCGGC
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Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559
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/mol type="genomic DNA"
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/mol type="taxon:39946"
/clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic |
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0; Mismatches 624; Indels
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Class: exon-trapped.
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Best Local S:
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KEYWORDS
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ORGANISM
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AUTHORS
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                      GCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGG 1451
                                                                    4245 GAAGCTGGAGGTGGTGACGTGGACAACGGCACCGACTACCGGCGCCCCACGCTGGAGCA 4304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:108607"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mastigamoeba balamuthi
Bukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (basea 1 to 867)
Bapteste, B., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
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The Rockefeller University
120 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
                                                                                                                     1452 CAAGCTGAACTGGGCCAGCCAGATCTACCC 1481
                                                                                                                                                                4305 GGTCCGGCTCTACCACTGCCCGCTGGGCCC 4334
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/strain="ATCC 30984"
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rockefell

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.
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Latshaw,S., Tan,B..C., Settles,A.M. and McCarty,D.R.
Sequence tagged transposon insertions from the UniformMu maize
                                                                                                                                                                                                                                                                                   Zea mays genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Florida
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1924
Sequence flanking probable Mu insertion site in UniformMu line: 0280349-08, Priner set: A
Class: transposon insertion site.
Location/Qualifiers
CL972913
CL982810
CL982362
CL962033
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Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
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                                                                                                                                                                                                                                                                         CL293849 330 bp DNA 02S0349-08A1-C03 UniformMu MuTAIL Library
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300,
Tel: 86-10-80481559
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/clone_lib="Oryza sativa
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Rice genomic sequence.
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone lib="Oryza sativa Express
/note="Oryza sativa exon trapped
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Pred. No. 2.8e-07;
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   Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Oryza sativa (indica cultivar-group)

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.

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May L., Wangc, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

L Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic
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Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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Department of Bioinformatic
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Chinese Academy of Sciences, Beijing 101300, China Fax: 86-10-80488559
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza, Liliopsida; Doales; Poaceae;
I (bases I to 1809)
Ma, L., Wangc, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
                                                                                               GGGGCTGGACAGGACTCGGTGCTCCTGTACGCGGCGAGGGGGCGTCCCGCGTCGAGAACCA
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Submitted (25-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  841 CTGTGGAACGGGTGCCCCTGCACCCGCCGTGTCCGCGCGTGTTTCCGCACCAGGGTCAAG
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/mol_type="genomic DNA"
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
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/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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                                                                                                                                                                                                                                                                                                                                                                                  Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
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1 (bases 1 to 951)
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1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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Laboratory of Biochemical Parasitology
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Bioinformatics
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, S7 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: [gas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software
This sequence is the direct result of the Base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [128,636].
Plate: Talt537 row: N column: 23.
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1 (bases 1 to 869)
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                                                               579 CGAGGAGACGACGACTGGCGTNATGAGGCTGTACCAGCTGCACCGCGACGGCAAGCTGCT
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CCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCTGAA
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                               An analysis of transcriptional regulation of the rists comparison to Arabidopsis
Unpublished (2004)
Unpublished (2004)
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China Pers: 86-10-80488676
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/db_xref="teaxon:39946"
/cloon=llb="cyrza sativa Express Library"
/note="Gryza sativa exon trapped genomic
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42.8%; Pred. No. 6.7e-05;
live 0; Mismatches 710;
and Wang, J.
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                  Email: chenchen@genomics.org.cn
Rice genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACGIGGGCGACGCCIACITCAGCGIGCCCTGGACGACGACITCCGCAAGIACACCGCC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1060 TTCACCATCCCCAGCATCAACAACGAGCCCCCGGCATCCGCTACCAGTACAACGTGCTG 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1120 CCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1180 CCCTTCCGCCCCCCCAACCCCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTG 1239
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Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantas, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza,
I bases I to 3069)
Ma.L., Wango,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhao,H., Yuan,L.,
                                                                                                                                                                                                                                                                                                                                                                                      768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 AAGTGGCGCAAGCTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAG 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smart
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                640 ATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCC
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                                                                                                                                                                                                                                      Gaps
       hardened at 2 C for 1 day (24 H) (driver). Modified cDNA (Clontech)priming and non-directional cloning
                                                                                                                                                                                                                                          ;
0
                                                                                                                                                    Length 869;
                                                                                                                                                    Score 85; DB 7; Length 869
Pred. No. 4.1e-05;
0; Mismatches 365; Indels
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CL973991.1 GI:52402507
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llarity 45.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  GATTGGTAGGAGGTTCTCCGACCCGTCCGTGCAGAGTGACATGAAGCTATGGCCGTTCAA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGCGCACGCTGTCGTCGACGGCGCAGACCACTTGAGATCGACTCGCTGTACGAGGG 884
                                                                                                                                                                                                                      CGCCGCCAAGAACCAGGTCGCCATGAACCCAACCAACACGTCTTCGATGCGAAGCGGTT
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                                                                                                                                                          Gaps
/note="Oryza sativa exon trapped genomic sequences
                                                                                                                                                          30;
                                                                                          Length 1941
                                                                                                                                                          Indels
                                                                                       Score 83.8; DB 9;
Pred. No. 7e-05;
0; Mismatches 992;
                                                                                              Query Match
3.4%;
Best Local Similarity 42.9%;
Matches 769; Conservative
                                                                                                                                                                                                                      267
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
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Ma.L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M.,
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Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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Rice genomic sequence.
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/ Forganism="MRNA"
/ Strain="ATCC 30984"
/ Gb xref="texon:108607"
/ Clone lib="Mastigamoeba balamuthi lambda ZAP II
/ note="syn: Phreatamoeba balamuthi"
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Liaboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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Mastigamoeba balamuthi
Bukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1132)
1 bases 1 to 1132)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
Philippe, H.
                                                                                                                              GCTGCGCAAGCACCTGCTGCGCTTGGGGCTTCACCACCCCGACAAGAAGCACCAGAAGGA
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.

1 (bases 1 to 867)
Bapteste,E., Brinkmann,H., Lee,J.A., Moore,D.V., Sensen,C.W., Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and Philippe,H.
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The Rockefeller University
1230 York Avenue, New York, NY 10021, U
Email: mmuller@rockvax.rockefeller.edu
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/etrain="ATCC 30984"
/db_xraf="taxon:108607"
/clone lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
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rockefeller.0.353 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to ribosomal protein L5, mRNA
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Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1165)
Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and Philippe, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                      919 GCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGCC
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1230 York Avenue, New York, NY 10021, University of the Manuller@rockwax.rockefeller.edu
Insert Length: 1165 Std Brror: 0.00
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Laboratory of Biochemical Parasitology
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Mastigamoeba balamuthi
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1 (bases 1 to 11691)
May.L., Wangv.J., Chen.C., Liu,X., Su,N., Li,L., Wang,X., Cao,
Juiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome its comparison to Arabidopsis
Unpublished (2004)
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42.2%; Pred. No. 0.00074;
tive 0; Mismatches 771; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Oryza sativa Express Library"
/note="Oryza sativa exon trapped genomic
                                                                                                                              Contact: Chen Chen
Department of Bioinformatic
Department of Bioinformatic
Chinnes Academy of Sciences, Beijing 101300,
Tel: 86-10-8048155
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa
/mol_type="genomic DNA"
/db_xref="taxon:39946"
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OBIFCC008219 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
CL962901.1 GI:52380530
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Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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/mol_type="mRNA"
/strain="ATCC 30994"
/db_xref="taxon:108607"
/clone_lib="Wastigamoeba balamuthi lambda ;
/note="syn: Phreatamoeba balamuthi"
                                                                                                                                    3.2%; Score 79; DB 4; Length 867, 45.7%; Pred. No. 0.00049;
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/organism="Oryza sativa (indica c
/mol type="genomic DNA"
/mol type="genomic DNA"
/Ob xref="texon:39946"
/clone lib="Oryza sativa Express
/note="Oryza sativa exon trapped
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 78.2; DB 9;
Pred. No. 0.00071;
); Mismatches 1013;
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Oryza sativa (indica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1962)
Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Vano,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L.,
Wong,G.K.S., Deng,X.W. and Wang,J.
      GGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAA
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, Chinà
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Search completed: June 2, 2005, 02:53:19 Job time : 7886.14 secs

Appli Appli

Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

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APPLICANT: Kang, Yong C.

TITLE OF INVENTION: Polypeptide having immunological

TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: KIRBY EADES GALE BAKER
                                                                                                                                                                                                                                                                                                                                    Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
Patent No. 5252477
Patent No. 5320958
                                                                                                                                                                                                            Sequence 5, Appli
Sequence 5, Appli
Patent No. 5223423
Patent No. 5223423
                                                                                                                                                                                                                                                           Sequence 1, Appli
Sequence 72, Appl
Sequence 71, Appl
Sequence 8, Ap
Sequence 7, Ap
Sequence 6, Ap
Sequence 22, A
Sequence 35, A
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Sequence 4, Al
Sequence 14, 1
Sequence 14, 1
Sequence 14, 1
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Sequence 24,
Sequence 16,
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.

REGISTRATION NUMBER: 28,584
REFERENCE/POCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      US-09-625-972-24
US-09-991-258-16
US-08-659-251-5
US-09-256-490-5
PCT-US96-11445-5
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US-08-444-882-6
US-08-389-459A-6
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US-08-679-493A-72
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                                    US-07-743-357-22
US-09-952-060-35
US-07-743-357-6
                                                                                   US-09-952-060-2
US-09-952-060-8
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                                                                                                                                                                                                                                      5223423-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ontario
COUNTRY: Canada
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07743357
Patent No. 5858646
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-0045
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                       RESULT 1
   June 2, 2005, 03:13:23 ; Search time 34 Seconds (without alignments) 10815.332 Million cell updates/sec
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/cgnz_6/ptodata1/iaa/backfiles1.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                            protein search, using frame_plus_n2p model
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US-07-743-357-9
US-09-124-900-3
US-08-463-028-9
US-09-309-57-2
US-09-309-572-17
US-07-743-357-5
US-07-743-357-3
US-07-743-357-3
US-07-743-357-3
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Result Š

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AAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGCACCCCGGCATCCGCTACCAG
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                                                                               ORGANISM: Human immunodeficiency virus type 1
                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1005 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                         1.22e-208
3497.00
95.56%
90.85%
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Best Local Similarity:
Query Match:
DB:
                                                                                     STRAIN: HXB2
.07-743-357-1
                                                                                                                  Alignment Scores:
Pred. No.:
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                                                                                                                                                                                                                                                                                              Sequence 9, Application US/07743357
; Sequence 9, Application US/07743357
; Patent No. 5858646
; GENERAL INFORMATION:
    APPLICANT: Kang, Yong C.
    TITLE OF INVENTION: Delypeptide having immunological
    TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
    NUMBER OF SEQUENCES: 22
    CORRESPONDENCE ADDRESS:
    CORRESPONDENCE ADDRESS:
    STREET: Box 3432, Station D
    COLTY: Ottawa
                                            CTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATC 2181
                                                                                          ATCCAGGCCCAGCCCGACAAGAGCGAGAGCGAGCTGGTGAACCAGGATCATCGAGCAGCTG 2241
                                                                                                                                       ATCAAGAAGGAGAAGGTGTACCTGAGCTGCCCGCCCCACAAGGGCATCGGCGAAC 2301
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ATCGTGAGCCTGACCGAGACCACCAGCAGAAGACCGAGCTGCAGCCGATCCAGCTGGCC
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION NUMBER: PCT/CA90/00062
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: PCT/CA90/00062
ATTONEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,584
REFRENCE/POCKET NUMBER: 30924-2
TELEPHONE: (613) 237-6900
TELEPHONE: (613) 237-6900
TELEPHONE: (613) 237-0045
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHRARACTERISTICS:
LENTH: 1003 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human immunodeficiency virus type 1 STRAIN: MAL US-07-743-357-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: K1M 1H8
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Asp 722
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US-07-743-357-9
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                              Conservative:
Mismatches:
Indels:
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   Length:
Matches:
 2.01e-208
3493.50
95.97%
90.56%
76.39%
                              Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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2245 AAGAAGGAGAAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAG
                                  2305 CAGATCGACAAGCTGGTGAGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
GOTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,210
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 06/693,866
PRIOR APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-0CT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leelie A.
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 35,353
REFRENCE/DOCKET NUMBER: 2026-4193US2
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUIENCE CHARACTERISTICS:
SEQUIENCE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GRANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
LOCATION: 1..1015
OTHER INFORMATION: /note= "pol protein of
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morgan & Pinnegan, L.L.P. STREET: 345 Park Avenue CITY: New York STATE: New York COUNTX: USA ZIP: 10154-0053
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       ; Sequence 9, Application US/08463210; Patent No. 6001977
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3475.00
93.72%
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarit
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301 AsnValLeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLys 320
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                                                  CTGTACGTGGGCAGCGTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGC
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Š	1306	TTCACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGTAGGAG 1365
q 0	381	
දි සි	1366	CTGCACCCCGACAAGTGGACCGTGCACCATCGACTGCCCGAGAAGGAGGGCTGGACC 1425
8	1426	GTGAACGACGACAGAGCTGGAGCAAGCTGAACTGGGCCAGCCA
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ò	1486	ATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGGCGCCAAGGCCCTGACCGACATCGTG 1545
qq	441	ileLysvalArgGlnLeuCysLysLeuLeuArgGlyThrLysAlaLeuThrGluValIle 460
ò	1546	CCCCTGACCGAGGCCGAGCTGGCGAGCTGGCGAGAACCGCGAGATCCTGCGCGAGCCC 1605
g G	461	ProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGluPro 480
<i>∂</i> 8	1606	GTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCCAGATCCAGAAGCAGGGC 1665
ò	1666	CACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAG 1725
QQ	501	GlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLyBAsnLeuLysThrGlyLys 520
ò	1726	TACGCCAAGATGCGCACCGCCCACCACCACGACGTGAAGCAGCTGACCGAGGCCGTGCAG 1785
qq	521	TyralaargMetargGlyalaHisThrAsnaspValLysGlnLeuThrGluAlaValGln 540
ò	1786	AAGATCGCCATGGAGATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATC 1845
q	541	LysileThrThrGluSerileValileTrpGlyLysThrProLysPheLysLeuProlle 560
ò	1846	CAGAAGAAGACCTGGGAGACCTGGTGGACCTACTGGCAGGCCACCTGGATCCCCGAG 1905
qq	561	GlnLysGluThrTrpGluThrTrpTrpThrGluTyrTrpGlnAlaThrTrpIleProGlu 580
ò	1906	TGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAGAGA
g	581	TrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluLysGluPro 600
È	1966	ATCATCGGCGCCGAGACCTTCTACGTGGACGCGCCCCAACGCGAGCACCCAAGATCGGC 2025
g G	601	ilevaldiyaladluThrPheTyrValAspGlyAlaAlaAsaArgGluThrLysLeuGly 620
B &	2026	AAGGCCGCTACGACCGACCGACCGGCGGCAGAAGATCGTGAGCCTGACCGACACCACC 2085
ò	2086	AACCAGAAGACCGAGCCGATCCAGCTGGCCCTGCAGGACAGGGGGGGG
q	641	
ò	2146	AACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGC 2205
qq	661	
۵,	2206	GAGAGCGAGCTGGTGAACCAGATCATCGAGCTGATCAAGAAGGAGGAGGTGTACCTG 2265
qq	681	GluSerGluLeuValAsnGlnIleIleGluGlnLeuIleLysLysGluLysValTyrLeu 700
8 8	2266	AGCTGGGTGCCCGCCACAAGGGCATCGCGGCGCAACGAGCAGATCGACAAGCTGGTGAGC 2325
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È	2326	AAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2364

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                                                                     381 LeuThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyrGlu
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 141 GlyThrValLeuValGlyProThrProValAsnIleIleGlyArgAsnLeuLeuThrGln
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|GlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGlnArgProLeuValThr
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                  LENGTH: 1015
TYPE: PRT
ORGANISM: Human imunodeficiency virus type 1
                                                                            JEGERRAL INC. 8.2.08184

APPLICANT: RATINGER, Hermann

APPLICANT: BUCHACHER, Andrea

APPLICANT: BUCHACHER, Andrea

APPLICANT: BALLAUN, Claudia

APPLICANT: BALLAUN, Claudia

APPLICANT: TRKOIA, Alexandra

APPLICANT: TRKOIA, Alexandra

APPLICANT: TRKOIA, Alexandra

APPLICANT: TRKOIA, Alexandra

APPLICANT: STEINDL, Renate

APPLICANT: STEINDL, Franz

APPLICANT: MUSTER, Thomas

APPLICANT: MUSTER, Thomas

APPLICANT: WISTER, 1939-112P

CURRENT APPLICATION NUMBER: US/09/124,900

CURRENT PILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: PCT/EP95/01481

PRIOR PILING DATE: 1995-04-19

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.0
                                                           Sequence 3, Application US/09124900
Patent No. 6268484
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3475.00
93.72%
89.22%
75.99%
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                gnment Scores:
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                                                 1786 AAGATCGCCATGGAGGATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATC 1845
                                                                                                  CAGAAGGAGACCTGGGAGCCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAG 1905
                                                                                                                                                    1906 TGGGAGTICGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCC 1965
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             661 AsnileValThrAspSerGlnTyrAlaLeuGlyIleileGlnAlaGlnProAspLysSer 680
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LyslleThrThrGluSerIleVallleTrpGlyLysThrProLysPheLysLeuProlle
                                                                                                                  TACGCCAAGATGCGCACCGCCCACACCAACGACGTGAAGCTGACCGAGGCGGTGCAG
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Sequence 9, Application US/08463028
Sequence 9, Application US/08463028
GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
TITLE OF INVENTION: CLONING AND EXPRESSION OF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
STREET: 345 Park Avenue
CITY: New York
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: USA
ZIP: 10154-0053
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101 LeuGluGluMetSerLeuProGlyArgTrpLysProLysMet11eGlyGlyIleGlyGly 120
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|GlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGlnArgProLeuValThr
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OTHER INFORMATION: /note= "pol protein of HTLV-III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 23-JAN-1985

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 758-4800
TELEFAN: (212) 751-649
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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3475.00
93.72%
89.22%
75.99%
                                                                                                                                                                                                                                                                                           LENGTH: 1015 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
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Best Local Similarity:
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APPLICANT: Kang, Yong C.

TITLE OF INVENTION: Polypeptide having immunological

TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D

CITY: Ottawa

STATE: Ontaxio

COUNTRY: Canada
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LysileThrThrGluSerileValileTrpGlyLysThrProLysPheLysLeuProile 560
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-191
CLASSIFICATION: 424
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REGISTRATION NUMBER: 28,584
REGISTRATION NUMBER: 28,584
REGISTRATION NUMBER: 28,584
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COUNTRY: Canada
ZIP: K1M 1H8
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TELEFAX: (613) 237-0045

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: internal
ORIGINALS. SOURCE:
ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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3475.00
93.72%
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Best Local Similarity:
                                                                                                            BH102
    TELEFAX:
INFORMATION FC
SEQUENCE CH-
EENGTH: 1
TYPE: ami
STRANDEDH:
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GACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGGCGGGCCTGAAGAAGAAGAAGAGG 987
  EP 99250415.9
                                                                            CTHER INFORMATION: pol polyprotein US-09-718-096-17
PRIOR APPLICATION NUMBER: EP 992
PRIOR FLLING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: US 09/
PRIOR PILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATCHILL VET. 2.0
SEQ ID NO 17
LENGTH: 1003
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Query Match:
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                                                                       Sequence 17, Application US/09718096
Patent No. 6589763
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
REFERENCE: 35-195
CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: D00-11-22
PRIOR PILING DATE: 1998-11-26
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                                                                                                           TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
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	601 AlaAsnArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLys	2062 ATGGTGACCTGACCGAGACCACCAGAGACCGGGGCTGCAGGCCATCCAGCTGGCC :::	2122 CTGCAGGACAGCGAGGTGAACATCGTGACGAGCAGTAGGCCTGGGCATCGTGACGAGTGAGCCTTGGGCATCGTGACGAGTGAGCAGTGAGCAGTGAGAGTGAGGCATCGTGACGAGTGAGAGTGAGAGTGAGGCAGTGAGAGTGAGGCAGTGAGAGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG		2242 681	2502 GACCAGATCGATCAGACTGGTCAGACTACCGATCCGATC	UY 2302 CM1 2304 Db 721 Asp 721	US-07-743-357-5 ; Sequence 5, Application US/07743357 ; Patent No. 5856900000000000000000000000000000000000	; GENERAL INFORMATION: ; TITLE OF INVENTION: Polypeptide having immunological ; TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine	CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSE: KIRBY EADES GALE BAKER STREET: Box 3432, Station D	; STATE: Ontawa; ; STATE: Ontario; COUNTRY: Canada; ZIP: KIM 1H8	COMPUTER KEADABLE FORM: MEDIUM TYPE: IBPOPO disk COMPUTER: IBP C compatible OPERATING SYSTEM: PC-DOS/MS-DOS COMPUTER: PC-DOS/MS-DOS	ntin Actease #1.0, ON DATA: BER: US/07/743,357 1-AUG-1991	; CLASSIFICATION: 424 ; PRIOR APPLICATION DATA; ; APPLICATION NUMBER: PCT/CA90/00062 ; FILING DATE: 23-FEB-1990 ; FILING DATE: 37-FEB-1990	HIGHER TAGE TOWN INCOME. NAME: Gale, Edwin J. REGISTRATION NUMBER: 28,584 REPREBRUCE/DOCKET WHOMER: 30924-2	TELEPHONE: (613) 237-6900 TELEPAX: (613) 237-0045 TOOLEFAX: (613) D.O. 5: TOOLEFAX: (613) D.O. 5: TOOLEFAX: (613) CONTENT OF TOOLEFAX: (613) CONTE	FIGURE CONTROLLED STATES TARREST TARREST TARREST TARREST TARREST TO THE STRANDEDNESS: not relevant	2 2 2	; ORIGINAL SOURCE: ; ORGANISM: Human immunodeficiency virus type 1 ; STRAIN: BRU
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                    Length:
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Mismatches:
Indels:
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                                        Local Similarity:
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220 TTCTTCGGGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTC	61 GlnGlyThrValSerPheAsnPheProGlnIl=	532 TTCATCAAGGTGCGCCAGTACGACAGATCCTGATCGGGGAAGAAGGCCATC 591	CTGGGCTGCACCCTG	772 CTGACCGCCATCTGCGAGGAGGAGGAGGAGGATCACCAAGATCGGCCCCGAG 831	892 CTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGC 951 [1012 GCCTACTTCAGCGTGCCCTGGACGAGCTTCCGCAAGTACACCGCCTTCACCATCCCC 1071	32 21 4 4 4 6
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Db 661 AsnileValThrAspSerGlnTyrAlaLeuGlylleIleGlnAlaGlnProAspLysSer 680 Qy 2206 GAGAGCGAGCTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAGGTGTACCTG 2265	RESULT 10 US-07-743-357-3 ; Sequence 3, Application US/07743357 ; Patent No. 585846 ; GENERAL INFORMATION: ; TITLE OF INVENTION: ; TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine ; NUMBER OF SEQUENCES: 22	CORRESPONDENCE ADDRESS: ADDRESSEE: KIRBY EADES GALE BAKER STREET: Box 3432, Station D CITY: Ottawa STATE: Ontario COUNTRY: Canada ZIP: KIM 118 COMPHER READAHUR FORM:	IUM TYPE: F PUTER: IBM RATING SYSTE TWARE: Pate NT APPLICATIO LICATION NUM LING DATE: 2 SSIFICATION:	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: PCT/CA90/00062 ; FILING DATE: 23-FBB-1990 ; ATTORNEY/AGENT INFORMATION: ; REGISTRATION NUMBER: 28,584 ; REFERENCE/DOCKET NUMBER: 30924-2 ; TELECOMMUNICATION INFORMATION:	ot: a 6:1813.6	; MOLECULE TEE: Protein ; MYPOTHETICAL: NO ; FRACMENT TYPE: internal ; ORIGINAL SOURCE: ; STRAIN: Human immunodeficiency virus type 1 ; STRAIN: BH5	Alignment Scores: 7.66e-207 Length: 1016 Pred. No.: 3468.00 Matches: 652 Score: 3468.00 Matches: 35 Best Local Similarity: 93.72% Conservative: 35 Best Local Similarity: 88.95% Mismatches: 28 Query Match: 75.84% Indels: 18 DB: 2 Gaps: 4 US-09-610-313B-31 (1-2463) x US-07-743-357-3 (1-1016)

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APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: KIM 1H8
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC Compatible
COMPUTER: Plan PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION 1424
PRIOR APPLICATION DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/POCKET UNMBER: 30924-2
TELEPHONE: (613) 237-6900
TELEFAK: (613) 237-6900
TELEFAK: (613) 237-0045
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
   721 AlaGlyIleArgLysIleLeuPheLeuAspGlyIleAsp 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1
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Matches:
Conservative:
Mismatches:
Indels:
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                                      Sequence 4, Application US/07743357; Sequence 4, Application US/07743357; Patent No. 5858646; GENERAL INFORMATION:
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3465.00
93.72%
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STRANDEDNESS: no
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                          161 ThrvalProvalLysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeu
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COUNTRY: Canada

ZIP: KIM 1H8

COMPUTER READABLE PORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/O7/743,357

FILING DATE: 21-AUG-1991

CLASSIFICATION NUMBER: US/O7/743,357

FILING DATE: 23-FEB-1990

ATYORNEY/AGENT INPORMATION:

NAME: Gale, Edwin J.

REGISTRATION NUMBER: 28,584

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REGISTRATION NUMBER: 28,584

REGISTRATION NUMBER: 217-6900

TELEFPHONE: (613) 237-6900

TELEFPHONE: (613) 237-6900

TELEFRAX: (613) 237-0045

INPORMATION POR SEQ ID NO:

LEMCTH: 1003 amino acids
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Conservative:
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  BAKER
3: KIRBY EADES GALE
Box 3432, Station D
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95.28%
89.72%
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                                                                  Ontario
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                    ORGANISM: Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
 APPLICATION NUMBER: PCT/CA90/00062
        FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: GALO. Edwin J.
REGISTRATION NUMBER: 28-584
REFERENCE/DOCKET NUMBER: 30924
TELECHOMICATION INFORMATION:
TELEPHONE: (613) 237-690
TELEFAX: (613) 237-690
TELEFAX: (613) 237-690
TELEFAX: (613) 237-695
INFORMATION FOR SEQ ID NO: 8: SEQUENCE TRANSPERISTICS:
LENGTH: 1003 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
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; Patent No. 5858646
; GENERAL INFORMATION:
    APPLICANT: Kang, Yong C.
    TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
    NUMBER OF SEQUENCES: 22
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: KIRBY EADES GALE BAKER
; STREET: Box 3432, Station D
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STATE: Ottawa
STATE: Ottawa
STATE: Ottawa
COUNTRY: Canada
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 21-AUG(1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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US-07-743-357-8
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Matches:
Conservative:
Mismatches:
Indels:
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                     ORGANISM: Human immunodeficiency virus type STRAIN: SF2
-07-743-357-7
                                                           1.15e-205
3449.00
94.87%
89.60%
 HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
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                                                    Alignment Scores:
Pred. No.:
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US-09-952-060-4
US-09-117-217-14
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                              protein search, using frame_plus_n2p model
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AAGATCCTGGAGCCCTTCCGCGCCCCCAACCCCGAGATCGTGATCTACCAG-----GCC 1221
                           TyrabnValLeuProGlnGlyTrpLysGlySerProAlallePheGlnSerSerMetThr
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ProPheLeuTrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleVal
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Mismatches:
Indels:
Gaps:
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                                                                             Human immunodeficiency virus type
SEQUENCE CHARACTERISTICS:
LENGTH: 1005 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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95.01%
90.29%
75.83%
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Best Local Similarity:
Query Match:
DB:
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US-07-743-357-1
                                                                            ORGANISM:
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Pred. No.:
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15 Sequence 9, Application US/07743357

15 Fatent No. 585864

16 GENERAL INFORMATION:

17 TILE OF INVENTION: Polypeptide having immunological

17 TILE OF INVENTION: activity for use as diagnostic reagent and/or vaccine

17 TILE OF INVENTION: activity for use as diagnostic reagent and/or vaccine

17 TILE OF INVENTION: activity for use as diagnostic reagent and/or vaccine

17 TILE OF INVENTION: activity for use as diagnostic reagent and/or vaccine

17 TILE OF INVENTION: activity for use as diagnostic reagent and/or vaccine

18 STREET: Box 342, Station D

18 STREET: Box 342, Station D

19 CITY: Ottawa STREET: Box 342, Station D

21 FILE CANDITOR IN THE STREET: Box 342, Station D

21 COUNTRY: Canada

21 PRIOR FEADER FORM: REPORPY disk

MEDIUM TYPE: abtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: A204-1991

CLASSIFICATION NUMBER: PCT/CA90/00062

17 FILING DATE: 21-A04-1991

18 RETERNICS/DOCKET NUMBER: 28-590

18 RETERNICS/DOCKET NUMBER: 28-590

18 RETERNICS/DOCKET NUMBER: 29-690

19 RESERNICS/DOCKET NUMBER: 21-690

10 TELEPKN: (613) 237-690

10 TELEPKN: (613) 237-690

10 TELEPKN: (613) 237-690

11 TELEPKN: (613) 237-690

17 TELEPKN: (613) 237-690

18 TELEPKN: (613) 237-
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662 IleGlnAlaGlnProAspGlnSerGluSerGluLeuValAsnGlnIleIleGluGlnLeu 681
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                                                                CTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATC
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STRANDEDNESS: no
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                      US-09-610-313B-32 (1-2457) x US-07-743-357-9 (1-1003)
                                                             Gaps:
 1.63e-207
3450.50
95.42%
90.00%
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DNA

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2239 AAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAG
                                   CAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
                                                                                                                                                                                      Sequence 9, Application US/08463210
Patent No. 6001977
GENERAL INFORMATION:
APPLICANT: GALLO, Robert C.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: 1..1015
; OTHER INFORMATION: /note= "pol protein of HTLV-III"
US-08-463-210-9
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MEDIUM TYPE: Flopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,210
FLING DATE: 05-JUN-1995
CLASSIPICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
FRILNG DATE: 13-GCT-1984
FILING DATE: 10-GCT-1984
ATTORNEY/AGRAT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 32026-4193US2
TELECOMMULICATION INFORMATION:
THE TERMINE AND THE TELECOMMULICATION INFORMATION:
THE TELECOMMULICATION INFORMATION:
THE TERMINE AND THE TELECOMMULICATION INFORMATION:
THE TELECOMMULI
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HTLV-III
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Best Local Similarity:
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 GlyThrValLeuValGlyProThrProValAsnIleIleGlyArgAsnLeuLeuThrGln 160
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                                  AsnProTyrAsnThrProValPheAla1leLysLysLysAsSSsrThrLysTrpArgLys
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                       CTGGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACGTGCCCGTGAAGCTGAAG
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                                                               CCCGGCATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACGGAGGAGAAGATCAAGGCC
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                     APPLICANT: RATINGER, Hermann
APPLICANT: RATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: ERNST, Wolfgang
APPLICANT: ERNST, Wolfgang
APPLICANT: BALLAUN, Claudia
APPLICANT: TRKOLA, Alexandra
APPLICANT: TRKOLA, Alexandra
APPLICANT: TRKOLA, Annelies
APPLICANT: KLIMA, Annelies
APPLICANT: SCHWATZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: STEINUL, Franz
APPLICANT: HIV-Vaccines
TITLE OF INVENTION: HIV-Vaccines
TITLE REFERENCE: 1939-112P
CURRENT FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 3
LENTH: 1015
                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Human imunodeficiency virus type
                                                    Sequence 3, Application US/09124900
Patent No. 6268484
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93,18%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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NAME/KEY: Protein
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|JyslleThrThrGluSerIleVallleTrpGlyLysThrProLysPheLysLeuProIle
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                                                  AAGATCGCCATGGAGGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGCCTGCCCATC
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; Sequence 9, Application US/08463028
; Patent No. 6610476
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAL, Flossie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OP SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2320 AAGGCCATCCGCAAGGTGCTGTTCCTGGACGCCATCGAT 2358
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STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIPICATION: 435
FRUCR APPLICATION DATE:
APPLICATION NUMBER: US 06/693,866
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OTHER INFORMATION: /note= "pol protein of HTLV-III'
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FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leelie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
TELEFONE: (212) 758-4800
TELEFAN: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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3432.00
93.18%
88.68%
75.35%
                                                                                                                                                                                                                                                               LENGTH: 1015 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                    Human immunodeficiency virus type
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficie
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3432.00
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Best Local Similarity:
Query Match:
DB:
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 TELBFAX:

INFORMATION FO
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LENGTH: 1
TYPE: ami
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Mismatches:
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Sequence 17, Application US/09309572

Patent No. 6440730

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Retroviral hybrid vectors psering of the control of the control
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Patent No. 6589763
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV FILE REFERENCE: 35-195
CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 1998-11-26
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Matches:
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                                                                                                                                            type
       APPLICATION NUMBER: EP 99250415.9
                                                                                                                       TYPE: PRT
ORGANISM: Human immunodeficiency virus
                                                                                                                                                                     OTHER INFORMATION: pol polyprotein
PRIOR APPLICATION NUMBEK: DE CONTROL PRIOR FILING DATE: 1999-11-25
PRIOR PELING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 17
LENGTH: 1003
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3429.00
94.59$
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Best Local Similarity:
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Pred. No.:
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US-09-718-096-17
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RESULT 9
US-07-743-357-5
i Sequence 5, Application US/07743357
j Sequence 5, Application US/07743357
j Sequence 5, Application US/07743357
j Fatent No. 5858646
j GENERAL INFORMATION:
j TITLE OF INVENTION: Polypeptide having immunological
j TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
nUMBER OF SEQUENCES: 22
j CORRESPONDENCE ADDRESS:
j ADDRESSE: KIRBY EADES GALE BAKER
sTREET: Box 3432, Station D
cITY: Ottawa
cTATE: Ontario
 601 AlaAsnArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLys 620
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                            2056 ATCGTGAGCCTGACCGAGACCACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: KIM 148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-A04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1
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PRICR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STATEMENT ON TELEFAX: (613) 237-0945
INFORMATION FOR SEQ ID NO: 5:
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HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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261 ValThivalLeuAspValGlyAspAlaTyrPheSerValProLeuAspLysAspPheArg
                                                                                            AAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAG
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                            ATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGGGGGGCCCAAAGGCCCTGACCGACATCGTG
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APPLICATT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE 22 22 11/2 for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: KIRRY EADES GALE BAKER
STREET: Ontawa
STREET: Ontawa
STREET: Ontawa
STREET: Ontawa
STREET: Ontawa
STREET: ALM IHB
COMPUTER HEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ReacherIn Release #1.0, Version #1.30
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CLASSIFICATION DATA: 244
APPLICATION NUMBER: PCT/CA90/00062
FTLING DATE: 23-FEB-199
ATTORNEY/GAST INFORMATION:
NAME: Gale, Edwin 1 NYORMATION:
NAME: Gale, Edwin 1 NYORMATION:
TELEFONE: (G13) 237-0045
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TTREETERX: DATE FOR THE CONTINE THE CONTINE STRANDENESS: not relevant
MOLECHIS PYPE: POTCH in
                                                   700
                                                                                            661 AsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLysSer 680
                                         2260 AGCTGGGTGCCCGCCCACAAGGGCATCGGCGCAACGAGCAGATCGACAAGCTGAGC
                        2200 GAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTG
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                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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US-07-43-357-3
; Sequence 3, Application US/07743357
; Patent No. 5858646
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3425.00
93.18%
88.40%
75.19%
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HYPOTHETICAL: NO
PRAGMENT TYPE: internal
ORIGINAL SOURCE:
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Query Match:
DB:
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Pred. No.:
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Sequence 4, Application US/07743357
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: KANG, YONG C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----cccagcagcagaaccgcgcccaacagccccaccagc 303
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CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATFORNEY AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 30924-2
TELEPHONE: (613) 237-6900
TELEPHONE: (613) 237-6900
TELEPHONE: (613) 237-0045
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENDERAL 1016 amino acids
    721 AlaGlyIleArgLysIleLeuPheLeuAspGlyIleAsp 733
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                 ADDRESSEE: KIRBY BADES GALE BAKER
STREET: Box 3432, Station D
                                                                                                                                                                                                                                        COUNTRY:
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
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TOPOLOGY: not relevant
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3422.00
93.18%
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NO
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STRANDEDNESS: no
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Best Local Similarity:
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                                                                                                                                                                                                              CITY: Ottawa
STATE: Ontari
COUNTRY: Cana
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                                              US-07-743-357-4
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501 GlnGlyGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeuLysThrGlyLys 520
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TICCTG-----CCCATCGAGCTGCACCCGACAAGTGGACCGTGCAGCCCATCGAGCTG 1398
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                 571 ATCTGCGGCAAGAAGGCCATCGGCACCGTGATCGGCCCCACCCCCGTGAACATCATC
                                                              GGCCGCAACATGCTGACCCCAGCTGGCTGCACCCTGAACTTCCCCCATCAGCCCCATCGAG
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                                                                                                                                                                                                                                                                                                    TTCTGGGAGGTGCAGCTGGCCATCCCCCACCCGCCGGCCTGAAGAAGAAGAGGCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGATCGGCGCCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAG
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Dox 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: KIM 1HB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AuG-1991
CLASSIFICATION NUMBER: US/07/743,357
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORWATION:
MARE: Gale, Edwin D.
REFERENCE/DOCKET NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 23,76900
TELEPHONE: (613) 237-690
TELEPHONE: (613) 237-696
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TVDENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1003
642
40
31
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Mismatches:
Indels:
Gaps:
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Matches:
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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94.72%
89.17%
75.01%
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Best Local Similarity:
Query Match:
DB:
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HYPOTHETICAL: NO
FRAGMENT TYPE: IN
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APPLICATION NUMBER
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-07-743-357-8
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Sequence 8. Application US/07743357

Patent No. 5858646

GENERAL INFORMATION:

APPLICANT: Kang, Yong C.

TITLE OF INVENTION: Polypeptide having immunological

TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER

STREET: Box 3432, Station D

CITY: Octawa

STREET: Ontaxio
                                                                                                                                                1998
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                                                                     CAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACC 1818
                                                                                                          CCCAAGTICCGCCTGCCCATCCAGAAGGAGCACCTGGGAGACCTGGTGGACCACTACTGG 1878
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                                                                                                                     STATE: Ontario
COMPRY: Canada
ZIP: KHM 148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 21-ANG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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US-07-743-357-8
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643
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels:
PCT/CA90/00062
         FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28-584
REFERENCE/DOCKET NUMBER: 30924
TELECHONIO INFORMATION:
TELECHONE: (613) 237-690
TELEFAX: (613) 237-695
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                               3.34e-205
3413.50
94.72%
89.31%
                                                                                                                                                                                                                                                          FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
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Sequence 7, Application US/07743357
Patent No. 589846
GENERAL INFORMATION:
APPLICANT: APPLICANT:
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Octawa
STREET: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCCCCCC
                                                                                                        CAGGACAGCGCCCCTGGCTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATC
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: EN PC COMPATIBLE
COMPUTER: THE PC COMPATIBLE
COMPUTER: PACTORING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 36984
REFERENCE/DOCKET NUMBER: 36924-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (613) 237-6900 TELEPAX: (613) 237-0045 INFORMATION FOR SEQ ID No. 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1004 amino acids
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: Canada
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                                                                                                                                             TTCTGGGAGGTGCAGCTGGGCATCCCCCACCGCCGGCCTGAAGAAGAAGAAGAGCGTG 990
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PheLeuTrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleValLeu 400
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ATCACCAAGATCGCCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAG 870
                               GCCGAGATCCAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTC
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                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                     US-09-610-313B-32 (1-2457) x US-07-743-357-7 (1-1004)
                  type
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficiency virus
US-07-743-357-7
                                                                          Gaps:
                                            9.82e-205
3406.00
94.31%
89.04%
74.77%
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Best Local Similarity:
Query Match:
DB:
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                                         CTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGCCATCGGCGGCTTCATCAAGGTGCGC
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APPLICANT: ASSISTANCE FUBLIQUE-HOPITAUX DE LA RECHERCHE MEDICALE-INSERM
APPLICANT: ASSISTANCE FUBLIQUE-HOPITAUX DE PARIS
APPLICANT: INSTITUT PASTEUR
APPLICANT: LOUSSERT-AJAXA, Ibtissam
APPLICANT: ANDIALTANA, Ibtissam
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Francoise
APPLICANT: SARAGOSTI, Francoise
APPLICANT: SARAGOSTI, Sentob
APPLICANT: SARAGOSTI, Francoise
CURRENT PILING DATE: 1990-12-09
BRIOR APPLICATION NUMBER: FR96/15087
PRIOR APPLICATION NUMBER: FR96/15087
PRIOR APPLICANTON OF SEQ ID NOS: 98
SOFTWARE: PALENTIN VET. 2.1
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                                                                                                                                  GAGCAGATCGACAAGCTGGTCAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGCCATC 2355
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DE PARIS
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Human immunodeficiency virus type
                                                                                                                                                                                                                                                            Sequence 6, Application US/09319588C Patent No. 6509018
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3140.50
89.70%
79.53%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                    GAT 2358
                                                                                                                                                                                                            721 Asp 721
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; ORGANISM: Hum
US-09-319-588C-6
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                                                                                        GAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAAC
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2, 2005, 05:13:50 Search completed: June Job time: 106.917 secs

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Sequence:

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Scoring table:

Minimum DB Maximum DB

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GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                Sequence 14, Appl
Sequence 14, Appl
Sequence 4, Appli
Sequence 14, Appli
Sequence 24, Appli
Sequence 16, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
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Sequence 6, Appli
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Sequence 9, Appli
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Patent No. 5320958
Patent No. 5320958
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                                                                                              Sequence 35,
Sequence 6, 7
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION NUMBER: PCT/CA90/00062
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 30-54-2
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5223423-4
US-09-69-493h-71
US-08-679-493h-71
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US-08-389-446-6
US-08-389-446-6
US-08-389-459h-6
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US-08-997-867h-6
US-09-238-309-9
US-09-248-309-9
US-07-743-357-8

US-07-743-357-7

US-09-319-586C-6

US-09-952-060-35

US-09-952-060-6

US-09-952-060-6

US-09-952-060-6

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; Patent No. 5858646
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TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 1:
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       Command line parameters:
-MODEL=frame+ n2p.model - DEV=xlh
-Q=/CORD_1/05PTO spool/US09610313/runat 31052005_155137_15173/app_query.fasta_1.7893
-Q=/CORD_2_1/USFPTO spool/US09610313/runat 31052005_155137_15173/app_query.fasta_1.7893
-D=/CORD_2_1/USFPTO spool/US09610313/runat 31052005_15317_15173/app_query.fasta_1.7893
-DSETSORES_DARGER=CORD_1 = NATRIEL = NATRIELS_DOSUM62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pct - THR MAX=100 - THR MINE O - ALIGN=15
-MODEL-COAL - OUTFMT=pcc - NORM=ext - HEAPSIZE=500 - WINLEN=0 - MAXLEN=200000000
-USER=US09610313 @CGN 1 1 101 @runat 31052005 155137 15173 - NCPU=6 - ICPU=3
-NO_MMAP - LARGEQUERY - NEG_SCORES=0 - WALT - DSPBELOK=10 - LONGLOG
-DSV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPEXT=0 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                                      June 2, 2005, 03:13:23 ; Search time 34.0828 Seconds (without alignments) 10815.332 Million cell updates/sec
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Sequence 9, P
Sequence 2, P
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Sequence 5, 7
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                              - protein search, using frame_plus_n2p model
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US-08-463-210-9
US-08-124-900-3
US-08-463-028-9
US-09-309-572-17
US-07-743-357-5
US-07-743-357-5
US-07-743-357-4
US-07-743-357-4
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Result

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CGCAAGCACCTGCTGCGCTTGGGGCTTCACCACCCCGGACAAGAAGCACCAGAAGGAGCCC 1347
                                                                                                  AAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCTACCAGTACATGGAC 1227
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AspPheTrpGluValGlnLeuGlyIleProHisProAlaGlyLeuLysLysLysSer
                                                                      TACAACGTGCCCCAGGGCTGGAAGGCCAGCCCCAGCATTTCCAGAGCAGCATGACC
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                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                     US-09-610-313B-30 (1-2469) x US-07-743-357-1 (1-1005)
                                                                 ORGANISM: Human immunodeficiency virus type STRAIN: HXB2
                    STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                   3.5e-213
3535.00
96.12%
91.40%
        : 1005 amino acids amino acids
 SEQUENCE CHARACTERISTICS
                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                       STRAIN:
-07-743-357-1
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Pred. No.:
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                                                                                                                                                                                                                                                                              Sequence 9, Application US/07743357
Fatent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
                                                                                    2247
                                         CTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATC 2187
                                                                                                                            GAGCAGATCGACAAGCTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGCCATC 2367
681
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                                                                                   2188 ATCCAGGCCCAGCCCGACAAGAGCGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
ATTONNEY/AGENT INPOMMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
CREANISM: Human immunodeficiency virus type
STRAIN: MAL
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CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (6.13) 237-6900
TELEFAX: (6.13) 237-0045
INFORMATION FOR SEQ ID NO: 9:
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LENGTH: 1003 amino acids
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STRANDEDNESS: not
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MOLECULE TYPE:
HYPOTHETICAL: N
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       Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              Gaps:
5.8e-213
3531.50
96.53$
91.11$
77.06$
                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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2311 CAGATCCACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
701 GlnValAspLysLeuValSerSerGlyIleArgLysValLeuPheLeuAspGlyIleAsg 720
                          2251 AAGAAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAG
                                                                                                                                                                                                                   EXPRESSION OF HTLV-III DNA
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OTHER INFORMATION: /note= "pol protein of HTLV-III"
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658
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/463,210
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Serunian, Leslie A.
REGISTRATION UNDBER: 35,353
REFERENCE/DOCKET UNDBER: 2026-4193US2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 05-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue
                                                                                                                                      Sequence 9, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: WONG-STAAL, Flossie
; TITLE OF INVENTION: CLONING AND EXI
; NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.35e-212
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89.77%
76.65%
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HVPOTHETICAL: NO
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COMPUTER READABLE FORM:
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STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New Yor
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                             US-08-463-210-9
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                         ATCCTGGAGCCCTTCCGGGCCCGGAACCCCGAGATCGTGATCTACCAGTACATGGACGAC 1230
                                                                                                                                                                               TTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCGAGCTG 1410
                                                                                                                                                                                                                                  CCCGAGAAGGAGACTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGG 1470
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                                                                                                                                           301 AsnValLeuProGlnGlyTrpLysGlySerProAlaIlePheGlnSerSerMetThrLys 320
                                         CTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACCGCCCCAAGATCGAGGAGCTGCGC
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                     261 IleProHisProAlaGlyLeuLysLysLysLysSerValThrValLeuAspValGlyAsp
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                 APPLICANT: RATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: BRIST, Wolfgang
APPLICANT: BALLAIN, Claudia
APPLICANT: BALLAIN, Claudia
APPLICANT: PURTSCHER, Martin
APPLICANT: PURTSCHER, Martin
APPLICANT: PURTSCHER, Renate
APPLICANT: SCHMATZ, Christine
APPLICANT: SCHMATZ, Christine
APPLICANT: KIIMA, Annelies
APPLICANT: STEINDL, Franz
APPLICANT: MUSTER, Thomas
ITILE OF INVENTION: HIV-Vaccines
ITILE OF INVENTION: 1939-112P
CURRENT PILLING DATE: 1939-07-30
PRIOR FILING DATE: 1995-07-30
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                           ORGANISM: Human imunodeficiency virus type
                                                    Sequence 3, Application US/09124900 Patent No. 6268484 GENERAL INFORMATION:
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3513.00
94.27%
89.77%
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Best Local Similarity: &
Query Match:
DB:
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Pred. No.:
                                                                                                                                                                                                                                                                                                       LENGTH: 1015
TYPE: PRT
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US-09-124-900-3
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| 521 TyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeuThrGluAlaValGln
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Sequence 9, Application US/08463028

Patent No. 6610476

GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, STALL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA NUMBER OF SEQUENCES: 1

NUMBER OF SEQUENCES: 1

CORRESPONDENCE SI

ADDRESSE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2332 AAGGCCATCCGCAAGGTGCTGTTCCTGGACGCCATCGAT 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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|GlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGlnArgProLeuValThr
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OTHER INFORMATION: /note= "pol protein of HTLV-III"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                 NAME: Serunian, Leslie A.
REGISTRATION VINDRER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
                                            US 06/659,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.35e-212
3513.00
94.27%
89.77%
76.65%
                                                                                                                                                                         TELEPHONE: (212) 756-4800
TELEFAX: (212) 751-6849
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 amino acids
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: HTLV-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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Query Match:
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Percent Similarity:
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APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
UNDBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               TGGGAGTTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAGGAGCCC
                                                                                                                                     ATCATCGGCGCCGAGACCTTCTACGTGGACGCGCCGCCAACCGCGAGACCAAGATCGGC
                                                                                                                                                                                     AAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Verse SOFTWARE: Patentin Release #1.0, Verse APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATE: 27-EB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
REFERENCE/DOCKET NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/07743357; Patent No. 5858646; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
COUNTRY: Canada
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy di
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|GlnGlyThrValSerPheAsnPheProGlnIleThrLeuTrpGlnArgProLeuValThr
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  TELEFAX: (613) 237-0045
; INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
CORGANISM: Human immunodeficiency virus type 1
STRANIS: BH102
US-07-743-357-2
                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                  US-09-610-313B-30 (1-2469) x US-07-743-357-2 (1-1016)
TELEFAX: (613) 237-0045
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1016 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHERICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Human immunodeficie
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Best Local Similarity: 8
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                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Retroviral hybrid vectors psering REPRIENCE: P50489
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER PILING DATE: 1999-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human immunodeficiency virus type
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US-09-309-572-17
Sequence 17, Application US/09309572
Patent No. 6440730
GENERAL INFORMATION:
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                                                                           TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
 EP 99250415.9
                    09/309,572
                                                                                                   ; OTHER INFORMATION: pol polyprotein US-09-718-096-17
PRIOR APPLICATION NUMBER: EP 992;
PRIOR FILING DATE: 1999-11-25;
PRIOR PELING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
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Patent No. 6589763
GENERAL INFORMATION:
APPLICANT: Von Laar, Meike-Dorothee
TITLE OF INVERTION:
FILE REFERENCE: 35-195
CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 1998-11-26
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Mismatches:
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                     1.98e-211
3507.00
94.41%
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                            Score:
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Db 661 AsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspLysSer 680 Qy 2212 GAGAGCGAGCTGGACCAGATCATCGAGCAGCTGATCAAGAAGGTGTACCTG 2271 [RESULT 10 US-07-743-357-3 ; Sequence 3, Application US/07743357 ; Patent No. 5856646 ; GENERAL INFORMATION: ; APPLICANT: Kang, Yong C. ; TITLE OF INVENTION: Polypeptide having immunological ; TITLE OF ENVENTION: activity for use as diagnostic reagent and/or vaccine	CORRESPONDENCE ADDRESS: ADDRESSE: KIRBY EADES GALE BAKER STREET: Box 3432, Station D CITY: Ottawa STATE: Ontario COUNTRY: Canada ZIP: KIM 118	MEDIUM TYPE: FORM: MEDIUM TYPE: I FORM; COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PILING DATE: 21-AUG-1991 CLASSIFICATION: 424-1991	18 5 7 3 5 1	TELEPHONE: (613) 237-6900 TELEPAT: (613) 237-6906 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1016 amino acids TYPE: amino acid classification of the sequent of strandom of sequence of sequent o	HYPOTHERICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE: STRAIN: Human immunodeficiency virus type 1	Alignment Scores: 2.29e-211 Length: 1016 Pred. No.: 3506.00 Matches: 656 Score: 650 Bercent Similarity: 94.27\$ Conservative: 35 Best Local Similarity: 89.50\$ Mismatches: 26 Query Match: 76.50\$ Indels: 16 DB: 2 Gaps: 3 US-09-610-313B-30 (1-2469) x US-07-743-357-3 (1-1016)

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APPLICANT: Kang. Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Oncario
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 31-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 30924-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
    721 AlaGlyIleArgLysIleLeuPheLeuAspGlyIleAsp 733
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                          RESULT 11
US-07-743-357-4
Sequence 4, Application US/07743357
Patent No. 5858646
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1016 amino acids
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COUNTRY: Canada
ZIP: KIM 118
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity:
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HYPOTHETICAL:
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ADDRESSEE: KIRBY EADES GALB BAKER
STREET: Box 3432, Station D
CITY: Octawa
STREET: Canada
STREET: Canada
COUNTRY: Canada
ZIP: KIM 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-PEB-1990
ATPOLICATION NUMBER: 28,584
FRIOK APPLICATION NUMBER: 28,584
FRIENEWEY/AGENT INFORMATION:
AMAME: Gale, Edwin J.
REGISTRATION NUMBER: 28,584
FRIENEWEY/DOCKET NUMBER: 28,584
FRIENEWEY/DOCKET NUMBER: 23-PEB-1990
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEFRAX: (613) 237-6900
TELEFRAX: (613) 237-0045
INFORMATION POR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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3497.50
95.83%
90.28%
76.31%
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HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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Best Local Similarity:
Query Match:
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STRAIN:
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Sequence 8, Application US/07743357

Sequence 8, Application US/07743357

Sequence 8, Application US/07743357

GENERAL INFORMATION:

APPLICANT: Kang, Yong C.

TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine TITLE OF INVENTION: activity for use as diagnostic reagent and/or vaccine NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: KIRBY EADES GALE BAKER

STREET: Box 3432, Station D

CITY: Octawa

STATE: Ontario

COUNTRY: Canada

ZIP: KIM 1H8

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/07/743,357

FILING DATE: 21-AUG-1991

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
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GTGAGCCTGACCGAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTG
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21 ThrArgAlaAsnSerProThrArgArgGluLeuGlnValTrpGlyArgAspAsnSerLeu 40
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human immunodeficiency virus type
               FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J.
REGISTRATION NUMBER: 30924-2
REGISTRATION NUMBER: 30924-2
TELEPHONE: (613) 237-6900
TELEFAX: (613) 237-6900
TELEFAX: (613) 237-6900
TELEFAX: (613) 237-6045
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1003 amino acids
TYPE: increase
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
APPLICATION NUMBER: PCT/CA90/00062
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        LysTyrThrAlaPheThrIleProSerIleAsnAsnGluThrProGlyIleArgTyrGln
                                                          GACCTGTACGTGGGCGACCTGGAGATCGGCCAGCACCGCGCCCAAGATCGAGGAGCTG
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                             TACAACGIGCICCCCAGGGCIGGAAGGCCAGCAGCCATCIICCAGAGCAGCAIGACC
                                     CTGCCCGAGAAGGAGGTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAAC
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                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                 US-07-743-357-7 (1-1004)
                        type
                       virus
                 : Human immunodeficiency
SF2
                                                            3.52e-210
3487.00
95.42%
90.15%
76.09%
 HYPOTHETICAL: NO FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                 US-09-610-313B-30 (1-2469) x
                                                   Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                       ORGANISM:
STRAIN: SF
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APPLICANT: Swanstrom, Ronald Ivar
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APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Worris, Lynn
APPLICANT: Wailiamson, Carolyn
TITLE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, Selected H
TITLE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
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TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
TITLE OF INVENTION NUMBER: PCT/IB01/01208
PRIOR APPLICATION NUMBER: DS 00/216,995
PRIOR FILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-10
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PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
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Publication No. US20040116660A1
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Query

Result

Sequence 118, App Sequence 88, Appl Sequence 3, Appli

Sequence 12, Appl Sequence 1, Appli Sequence 29, Appl

Sequence 14, Assequence 14, Bequence 10, Bequence 10, Bequence 10, Bequence 10, Bequence 10, Bequence 14, Asequence 1, Ase

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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
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                                                  GAGGCCGCCCGAGCGCCAGGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGC
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APPLICANT: Swanetrom, Ronald Ivar
APPLICANT: Swanetrom, Ronald Ivar
APPLICANT: Morris, Lynn
APPLICANT: Morris, Lynn
APPLICANT: Marim, Salim Abdool
APPLICANT: Williamson, Carolyn
TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives I TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives I FILE REFERENCE: 45669-281993
CURRENT APPLICATION NUMBER: US/10/312,413
CURRENT FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: A 2000/3437
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 10
                                                                                                              |||::::||| AlaSerTrpArgLysGlyAspValLeuGlnGlyAspValGlyArgGlnGlyPheProSer 119
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCTGCTGGAAG-----
                                                                                                                                                                                                                         ; Sequence 10, Application US/10332413; Publication No. US20040116660A1; GENERAL INFORMATION:
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      APPLICANT: Walker, Bruce
TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (IV9) COMPOUNDS
FILE REPERENCE: GZ 2112.00
CURRENT APPLICATION NUMBER: US/10/283,847
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 60/345,116
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
LENGTH: 1003
                                                                                                                                                                                                                           US-09-610-313B-30 (1-2469) x US-10-283-847-17 (1-1003)
                                                                                                                     ; ORGANISM: Human Immunodeficiency Virus
US-10-283-847-17
APPLICANT: Nicolette, Charles A.
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96.12%
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Sequence 17, Application US/10283847 Publication No. US20030162720A1 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: T cell leukemia-lymphoma virus (HTLV)
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFOCRATION:
APPLICANT: Chang, Nancy T
APPLICANT: Gallo, Robert C.
APPLICANT: Gallo, Robert C.
APPLICANT: Wong-Staal, Flossie
FILE NEPERENCE: 223695
CURRENT APPLICATION WUMBER: US/10/634,165
CURRENT APPLICATION WUMBER: 08/463,028
PRIOR APPLICATION WUMBER: 06/693,866
PRIOR FILING DATE: 1985-00-05
PRIOR FILING DATE: 1985-01-23
PRIOR FILING DATE: 1984-10-10
PRIOR FILING DATE: 1984-10-10
PRIOR FILING DATE: 1984-10-10
PRIOR FILING DATE: 1984-08-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PALENTIN VETSION 3.2
SOFTWARE: PALENTIN VETSION 3.2
SEMENT: 1015
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OTHER INFORMATION: /note= "pol
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TTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATC
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COTHER INFORMATION: protein encoded by construct of vaccine vector
COTHER INFORMATION: pGA2 and insert JS2 expressing clade HIV-1 VL
US-10-093-953A-26
                                                           APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Hua, Jian
APPLICANT: Hua, Jian
APPLICANT: Hua, Jian
APPLICANT: Mose, Bernard
APPLICANT: Mose, Bernard
APPLICANT: Myatt, Linda
APPLICANT: Wyatt, Linda
APPLICANT: Barl, Particia
TITLE OF INVENTION: AN INMUNE RESPONSE
FILE REFERENCE: 12804-005002
CURRENT APPLICATION NUMBER: US 60/186,364
PRIOR PELING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR APPLICATION NUMBER: US 09/798,675
PRIOR APPLICATION NUMBER: US 60/254,845
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-03-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR PELING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR PELING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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SEQ ID NO 26
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Matches:
Conservative:
Mismatches:
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US-10-093-953A-26
; Sequence 26, Application US/10093953A
; Publication No. US20040105871A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: protein encoded by construct of vaccine vector
OTHER INFORMATION: pGA1 and vaccine insert expressing clade B HIV-1
OTHER INFORMATION: Gag-Pol
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Matches:
              PRIOR APPLICATION NUMBER: PCT/USO1/06795
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/324,845
PRIOR PILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 739
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   FILING DATE: 2001-03-02
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Best Local Similarity:
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                                                                                                                                                                                                           Sequence 31, Application US/10093953A

Publication No. US20040105871A1

Sequence 31, Application US/10093953A

Publication No. US20040105871A1

GENERAL INFORMATION:

APPLICANT: Romith, James M.

APPLICANT: Hua, Jian

APPLICANT: Myatt, Linda

APPLICANT: Wyatt, Linda

APPLICANT: Exama

APPLICANT: Wyatt, Linda

APPLICANT: Wyatt, Linda

APPLICANT: Baral, Patricia

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING

TITLE OF INVENTION: COMPOSITION SAND METHODS FOR GENERATING

TITLE OF INVENTION: UNMBER: US 60/186,364

PRIOR APPLICATION NUMBER: US 60/251,083

PRIOR APPLICATION NUMBER: US 60/251,083

PRIOR APPLICATION NUMBER: US 60/251,083

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14. COCOLOGO COCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	1408 CTGCCCGAGAAGGAGCTGGACCGTGAACGACATCCAGAAGCTGGGGCAAGCTGAAC 1467		GCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGCGAGGCTGGAGCTGGCCGAG 158	164 480	1648 GTGGCCGAGATCCAGAAGCAGGGCCACGACCGACTGACCAGATCTACCAGGAGCCC 1707 :::	1708 TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCACCACCACCACCACGACGTG 1767 	1768 AAGCAGCTGACCGAGGCCGTGCAGAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG 1827 	1828 ACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAAGACCTGGTGGACTAC 1887 	1888 TGGCAGGCCACCTGGATCCCGAGTGGGAGTTCGTGAACACCCCCCCC	0 0	2008 GCCAACCGGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACC		CCAGTACGCCCTGGGCATC 		2248 ATCAAGAAGGAGAAGGTGTACCTGAGCTGGCTGCCCCCCCACAAGGGCATCGGCGGCAAC 2307 	2308 GAGCAGATCGACAAGCTGGTGAGCAACGCGAAGGTGCTGTTCCTGGACGGCATC 2367 :::	2368 GAT 2370 ::: 721 Glu 721	SULT 8 1-10-325-468-35 Sequence 35, Application US/10325468 Publication No. US20040101823A1 GENERAL INFORMATION:
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CCCTTCCTGTGGATGGGCTACGAGCTGCACCCGGACAAGTGGACCGTGCAGCCCATCGAG 1407
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                                                    GTGACCGTGCTGGACGTGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGC
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US-10-325-468-35
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## APPLICANT: Soong, Nay Wei

## APPLICANT: Pekrun, Katja

## APPLICANT: Pekrun, Katja

## APPLICANT: Pekrun, Katja

## APPLICANT: Shibata, Ritia

## TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS

## TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS

## TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS

## CURRENT APPLICATION NUMBER: US/10/325,468

## PRIOR APPLICATION NUMBER: US 60/343,524

## PRIOR PILING DATE: 2001-12-21

## NUMBER OF SEQ ID NOS: 56

## SOFTWARE: FastSEQ for Windows Version 4.0

## ILENGTH: 1003
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Matches:
Conservative:
Mismatches:
Indels:
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3466.00
95.28%
89.18%
                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: recombinant / chimeric sequence: clone 1.4 protein Pol;
OTHER INFORMATION: clone 1.26 protein Pol; clone P10.21 protein Pol;
OTHER INFORMATION: clone P10.26 protein Pol
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; Publication No. US20040101823A1
; GENERAL INFORMATION.
; APPLICANT: Soong, Nay Wei
; APPLICANT: Shibata, Ririi
; APPLICANT: Shibata, Ririi
; TITLE OF INVENTION: HODELS OF HIV-1 PATHOGENESIS
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; CURRENT APPLICATION NUMBER: US/10/325,468
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,524
; PRIOR PELLING DATE: 2001-12-21
; NUMBER OF SEQ 1D NOS: 56
; SEQ 1D NO 9
; SEQ 1D NO 9
; LENGTH: 1003
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US-10-325-468-20
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Sequence 20, Application US/10325468

Publication No. US20040101823A1

GENERAL INFORMATION:
APPLICANT: Scong, Nay Wei
APPLICANT: Scong, Nay Wei
APPLICANT: Scong, Nay Wei
TILLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
TILLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
TITLE OF INVENTION: 0DDELS OF HIV-1 PATHOGENESIS
FILE REFERENCE: 0166.210US
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/343,524

PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 56

SOFTWARE: PARESEC for Windows Version 4.0

SEQ ID NOS: 56
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10296734;
Publication No. US20040054137A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVERTION: Scott A
TITLE OF INVERTION: Synthetic molecules and use;
FILE REFERENCE: Savine
CURRENT FLING DATE: 2003-08-04
CURRENT FLING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SEQ ID NO 2
ILENGTH: 995
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Db 374 PheLeuTrpMetGlyTyrGluLeuHisProAspArgTrpThrValGlnProlleGluLeu 393 1411 CCCGAGAAGGAGACCTGAACGACATCCAGAAGCTGGTGGCAAGCTGAACTGG 1470	Oy 1651 GCCGAGATCCAGAGGCCACGACCAGCTGACCAGATCTACCAGGAGCCCTTC 1710 bb 474 AlaGluValGlnLysGlnGlyGlnAspGlnTrpThrTyrGlnIleTyrGlnGluProPhe 493 Oy 1711 AAGAACCTGAAGACGGCAAGATGCGCAAGATGCCCACCACCACGACGACGAAGG 1770 bb 494 LysAsnLeuLysThrGlyLysTyrSerArgLysArgSerAlaHisThrAsnAspValArg 513 Oy 1771 CAGCTGACGAGGCCGTGCAGAAGATGCCCATGGAGGATCGTGATCTGGGGCAAGACC 1830	Db 534		Oy 2251 AAGAAGGAGAAGTGTACCTGAGCTGCCCCCCACAAGGCCACGCAACGAG 2310 bb 674 LyeLysGluLysVallYrLeuSerTrpValProAlaHisLysGlyIleGlyGlyAsnGlu 693 Oy 2311 CACATCGACAGCTGGTAGCATCGCACCCCACAGGTGTTCCTGGACGGCTTCGTACGT 2370
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Conservative:
Mismatches:
Indels:
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  FILE OF INVENTION: Synthetic molecules and FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR PILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
LENGTH: 995
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NAME, KEY: MISC FEATURE LOCATION: (173). (173) OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
                                                             LOCATION: (48) ... (48) OTHER INFORMATION: X = unknown amino acid
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COCATION: (1947)..(194)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (255√). (255)
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OCATION: (280)..(281)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (320)...(320)
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X =
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                                                         594 SerArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysVal 613
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NAME/KEY: MISC_FEATURE
LOCATION: (15)...(15)
OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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ORGANISM: Artificial
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AAGAAGAGCGTGACCGTGGTGGACGTGGGGGGCCTACTTCAGCGTGCCCCTGGACGAG 1038
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21 Thr*****AsnSer***ThrSerArg***LeuTrpAspGlyGly**Asp****Leu
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                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (675)...(675)
OTHER INFORMATION: X = u
FEATURE:
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Query Match:
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                                     TACCACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCCACGACCAGTGGACC
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US-09-952-060-35
Sequence 35, Application US/09952060
Sequence 36, Application US/09952060
GENERAL INFORMATION:
APPLICANT: Emini, Emilio A.
APPLICANT: Edini, Rima
APPLICANT: Chen, Ling
APPLICANT: Chen, Ling
APPLICANT: Shiver, John W.
APPLICANT: Shiver, John W.
APPLICANT: Coner, Timothy J.
APPLICANT: Casimiro, Danilo R.
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                ATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACC
                                         -----SerLeuPhedlyAsnAspProSerSerGlnMetAla----
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                  AND
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADEMOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF
TITLE OF INVENTION: MODIFICATIONS
TITLE POPULATION: MODIFICATIONS
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT PELING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
PRIOR PLILOR DATE: 2001-09-07
PRIOR PELING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-15
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Mismatches:
Indels:
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Matches:
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3135.50
81.29%
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68.42%
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Best Local Similarity:
Query Match:
DB:
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                                                                                  GAGACCTTCTACGTGGACGCCCCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTAC
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RT "MOLECULAr Cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from virus type 1 subtype C: a set of 23 full-length clones from RL Botswana.";

J. Virol. 73:4427-4432(1999).

C. --- SIMILARITY: Belongs to peptidase family A2.

EMBL; AF110975; AAD17135.1; --

DR RSP; P044885; JUJA.

GO: 00019012; C: virion; IEA.

GO; GO: 00019012; C: virion; IEA.

GO; GO: 00004577; F: DNA binding; IEA.

GO; GO: 00004577; F: DNA binding; IEA.

GO; GO: 00004523; F: Tibonuclease H activity; IEA.

GO; GO: 00004523; F: Tibonuclease H activity; IEA.

GO; GO: 00004523; F: RNA binding; IEA.

GO; GO: 00004523; F: RNA binding; IEA.

GO; GO: 00004524; F: RNA binding; IEA.

GO; GO: 00005740; F: transfereded activity; IEA.

GO; GO: 0000570; F: sinc ion binding; IEA.

GO; GO: 0000570; F: sinc ion binding; IEA.

GO; GO: 0000510; P: DNA recombination; IEA.

GO; GO: 0000510; P: DNA recombination; IEA.

GO; GO: 0000520; P: PRA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
MEDLINE=99214383; PubMed=10196340;
NOVIESKY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg I Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
                   0.06x4p0
0.09wf68
0.09wf68
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0.08wdc2
0.08wdc3
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
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QBADS7
QBADG3
QBADG13
QBADR1
QBADC5
QBADC5
QBADC13
QBADC13
QBADC13
QBADC13
QBADC13
QBADC13
                   O6X4P0
O9WF68
Q8ADZ9
Q8ADE9
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Q7SV20
Q8ADN7
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Q9WLJ3
Q8AD85
Q7SPT9
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Q8AD93
Q8AE23
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-MODEL=frame+ n2p.model - DBV=xlh
-MODEL=frame+ n2p.model - DBV=xlh
-Q=/cgn2_1/uSPTO_spool/US09610313/runat_31052005_155136_15147/app_query.fasta_1.7893
-Q=/cgn2_1/USFTO_spool/US09610313/runat_31052005_155136_15147/app_query.fasta_1.7893
-DBCALIGN=200 - TRNG=xlastan - SUFFIX=n2p.rup - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=h] council - ALIGH=5 - MODE=LOCAL
-UNITS=bits - START=1 - END=-1 - MATRIX=h] council - ALIGH=5 - MODE=LOCAL
-UNITS=bits - CONDM=ext - HEAPSIZE=500 - MINIEN=0 - MAXIEN=200000000
-USER=US09610313 @CGN 1 1 725 @runat_31052005 155136_15147 - NCPU=6 - ICPU=3
-NO WMAP - LARREQUERY - NEG SCORES=0 - WANT - DSPBELOKE=100 - LONGLOG
-DBV TIMEOUT=120 - WARN TIMEOUT=30 - THERADS=1 - XGAPEXT=0 - S-FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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                                                                                                                                                                                                                                         gtcgacgccaccatggccga......ggggctagcaccggtgaattc 2469
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Q9wf89 human i
Q9wf86 human i
Q9wf62 human i
Q6x498 human i
Q6x476 human i
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                        protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                          1612378 segs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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                                                                                                                                                                                                                                                               AIDS; Aspartyl protease; Core protein; Hydrolase; Polyprotein;
                                                                                                                                                                                                                                                                       Procease; RNA-directed DNA polymerase; Transferase.
SEQUENCE 1427 AA; 161059 MW; P3B0C741A1EFB10A CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                   Pept_Aspartic.
Pept_Asp AS.
Retrovir_matrix.
Retrovir_p17.
Retrov capsid C.
Retrov capsid Netrov capsid C.
Retrov capsid Netrov capsid C.
         Integrase C.
Integrase Zn N.
Peptidase A2.
InterPro; IPR000721; Gag p24.
InterPro; IPR001303; Integrase_C.
InterPro; IPR001309; Integrase_Zn N
InterPro; IPR001309; Integrase_Zn N
InterPro; IPR001995; Peptidase_AZ.
InterPro; IPR001909; Pept_Aspartic.
InterPro; IPR001909; Retrovir_matri
InterPro; IPR001916; Retrov capsid_InterPro; IPR008916; Retrov capsid_InterPro; IPR008916; Retrov capsid_InterPro; IPR00156; RNaseH.
InterPro; IPR001584; Rve.
InterPro; IPR001659; RVT.eonnect.
InterPro; IPR001661; RVT_thumb.
InterPro; IPR001661; RVT_thumb.
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTC 72
                                                       "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIDS; Aspartyl protesse; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protesse; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
                                                                                                                                                                                                       Missip, 194285; 10144.

R GO; GO:0014910; C:virion; IEA.

R GO; GO:0014910; F:aspartic-type endopeptidase activity; IEA.

R GO; GO:000820; F:nDA binding; IEA.

R GO; GO:000823; F:peptidase activity; IEA.

R GO; GO:000823; F:peptidase activity; IEA.

R GO; GO:000423; F:ribonuclasse H activity; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0001964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:00018070; F:Zinc ion binding; IEA.

R GO; GO:00018070; F:Zinc ion binding; IEA.

R GO; GO:0006210; P:RNA-dependent DNA replication; IEA.

R GO; GO:0006208; P:RNA-dependent DNA replication; IEA.

R InterPro; IPR001308; Integrase_C.

R InterPro; IPR001308; Integrase_C.

R InterPro; IPR001308; Integrase_Zn.

R InterPro; IPR001969; Pept_Aspartic.

R InterPro; IPR001969; Pept_Aspartic.

R InterPro; IPR001969; Retrovir_matrix.

R InterPro; IPR001969; Retrovir_matrix.
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Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink
Essex M.;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                     J. Virol. 73:4427-4432(1999).
-!- SIMIGARITY: Belongs to peptidase family A2.
BEMBL; AFI10974; AAD17126.1; -.
HSSP; P04585; JJIA.
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PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZAF C2HC, 2.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZF CCHC, 2.
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InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT-Lhumb.
InterPro; IPR001878; Znf-CCHC.
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Pfam; PF00077; RVP; 1.
Pfam; PF06078; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00698; zf-CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00540; Gag_D17; I.
Pfam; PF00660; Gag_D24; I.
Pfam; PF02022; Integrase_Zn; I.
Pfam; PF00075; RnaseH; I.
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91.08%
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InterPro; IPR002156;
InterPro; IPR001584;
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MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                         SECUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
"Molecular cloning and phylogenetic analysis of human immunodeficiency
virus type I subtype C: a set of 23 full-length clones from
                                                   GGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGCATCCGCAAGGTGCTG
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GO; GO:0019012; C:virion; IRA.
GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
GO; GO:0008233; F:DNA binding; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008233; F:RNA binding; IEA.
GO; GO:0004523; F:RNA binding; IEA.
GO; GO:0005723; F:RNA binding; IEA.
GO; GO:0005729; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0005709; F:transferase activity; IEA.
GO; GO:0005709; F:transferase activity; IEA.
GO; GO:0005709; F:transferase activity; IEA.
GO; GO:00062709; P:transferase activity; IEA.
GO; GO:00062709; P:tra
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01-NOV-1999 (TEXBLRE1. 12, Created)
01-NOV-1999 (TEXBLRE1. 12, Last sequence update)
01-NAR-2004 (TEXBLRE1. 26, Last annotation update)
01-MAR-201 polyprotein.
Human immunodeficiency virus 1.
Viruses, Retroid viruses; Retroviridae; Lentivirus.
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EMBL; AF110973; AAD17119.1; -.
HSSP; P04585; 1JLA.
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GO; GO: 00019012; C: virion; IEA.
GO; GO: 0001807; F: DNA binding; IEA.
GO; GO: 0001807; F: PNA binding; IEA.
GO; GO: 0001807; F: PNA binding; IEA.
GO; GO: 0001823; F: PEPtidase activity; II
GO; GO: 0001823; F: PERA binding; IEA.
GO; GO: 0001823; F: PERA binding; IEA.
GO; GO: 0001879; F: RINA binding; IEA.
GO; GO: 0001879; F: PETICELURAL molecule ac
GO; GO: 0001870; F: PETICELURAL
GO; GO: 0001871; P: DNA integration; IEA.
GO; GO: 0006210; P: PETICELURAL
GO; GO: 0006210; P: PETICELURAL
INTERPRO; IPR001037; Integrase C.
INTERPRO; IPR001095; PEPTIGASE AC.
INTERPRO; IPR001995; PEPTIGASE AC.
INTERPRO; IPR001999; RELTOVIT matrix.
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Retrov_capsid_N.
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InterPro; IRR000071; Retrovir_p17.
InterPro; IRR008916; Retrov capsid
InterPro; IRR008919; Retrov capsid
InterPro; IRR00186; RMsseH.
InterPro; IRR00186; RWse.
InterPro; IRR001884; RVse.
InterPro; IRR010669; RVT connect.
InterPro; IRR010661; RVT thumb.
InterPro; IRR010661; RVT thumb.
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J. Virol. 73:4427-4432(1999)
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Pfam; PF00607; Gag_D24; 1
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DR Pfam; PF00077; RVP; 1.

DR Pfam; PF00077; RVT 1; 1.

DR Pfam; PF00018; RVT Connect; 1.

DR Pfam; PF00117; RVT Chumb; 1.

DR Pfam; PF00198; ZCCCHC; 2.

DR PRINTS; PR00134; HIVIMATRIX.

DR PRINTS; PR00134; HIVIMATRIX.

DR PROSITE; PS00141; ASP PROTEASE; 1.

PROSITE; PS50175; ASP PROTEASE; 1.

R PROSITE; PS50175; ASP PROTEASE; 1.

R PROSITE; PS50175; CCCC; 2.

W POLYDROLEIN; Protease; Core protein; Hydrolase; Metal-binding; M AIDS; Aspartyl protease; Core protein; Hydrolase; Transferase; Zinc R Schriber Finger 1...
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T. Virol. 73:4427-4432(1999).

S. EMBL, API109612.

HSDP: Q70622; 1HVN.

GO; GO:0019012; C:virion; IEA.

GO; GO:000377; F:integrase activity; IEA.

GO; GO:0008907; F:integrase activity; IEA.

GO; GO:000823; F:peptidase activity; IEA.

GO; GO:000823; F:ribonuclease activity; IEA.

GO; GO:0004523; F:ribonuclease activity; IEA.

GO; GO:0003723; F:ribonuclease activity; IEA.

GO; GO:0003723; F:ribonuclease activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.
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SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
MOVITSKY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
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Human immunodeficiency virus 1.

Viruses; Retroid viruses; Retroviridae;

VCBI_TaxID=11676;
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PROSITE; PS00141; ASP PROTERTROV; 1.
PROSITE; PS50175; ASP PROTESBS; 1.
ASP PROSITE; PS50175; ASP PROTESBS; ASP PROTESPS; ASP PROSITE; PS00179; ASP PROTESPS; ASP P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTC
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006270; F:zinc ion binding; IEA.
GO; GO:0006310; P:DNA integration; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:000678; P:proteolysis and peptidolysis; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR001072; Gag_D24.
InterPro; IPR001095; Peptidase_Zn_N.
InterPro; IPR001995; Peptidase_Zn_N.
InterPro; IPR001995; Peptidase_Zn_N.
InterPro; IPR001995; Peptidase_Zn_N.
InterPro; IPR001999; Retrovi_capsid_C.
InterPro; IPR001999; Retrovi_capsid_C.
InterPro; IPR001999; Retrovi_capsid_C.
InterPro; IPR001919; Retrovi_capsid_C.
InterPro; IPR001919; Retrovi_capsid_N.
InterPro; IPR001569; Retrovi_capsid_N.
InterPro; IPR001659; RVTSe.
InterPro; IPR001669; RVT_connect.
InterPro; IRR010669; RVT_chunb.
InterPro; IRR010669; RVT_chunb.
InterPro; IRR010669; RVT_chunb.
InterPro; IRR010669; RVT_chunb.
InterPro; IRR01069; RVT_chunb.
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                                                                                           ProSerLysAspLeulleAlaGlulleGlnLysGlnGlyHisAspGlnTrpThrTyrGln
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                                       GTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGC
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1429 AA.

PRT;

PRELIMINARY;

Q6X4P8 Q6X4P8;

Q6X4P8 ID Q6 AC Q6

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SEQUENCE FROM N.A.

PubMac=1470249; DOI=10.1089/088922203771881220;

PubMac=1470249; DOI=10.1089/088922203771881220;

McCutchan F.E., Maayan S., Kim B., Zeira M., Ferrari G., Birx D.L.,

McCutchan F.E., The stronger of HIV type 1 subtype C sequences from Ethiopia, observed in full genome analysis, is not sustained in subgenomic regions.";

AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
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GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:000817; F:DNA binding; IEA.

R GO; GO:0008233; F:DNA binding; IEA.

R GO; GO:0008233; F:ribonuclease H activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005709; F:rinc ion binding; IEA.

R GO; GO:0006270; F:rinc ion binding; IEA.

R GO; GO:0006270; F:rinc ion binding; IEA.

R GO; GO:0006278; F:NNA accombination; IEA.

R GO; GO:0006278; P:PNA accombination; IEA.

R GO; GO:0006278; P:PNA accombination; IEA.

R GO; GO:0006278; P:PNA-dependent DNA replication; IEA.

R GO; GO:0006278; P:PNA-dependent DNA replication; IEA.

R GO; GO:0006278; P:PNA-dependent DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris M.E., Birx D.L.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                               Kim B., McCutchan F.B.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
05-JUJ-2004 (TrEMBLrel. 27, Created)
05-JUJ-2004 (TrEMBLrel. 27, Last sequence update)
05-JUJ-2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol tusion polyprotein (Fragment).
Human immunodeficiency virus 1.
                                                                                          Viruses; Retroid viruses; Retroviridae; Lentivirus
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InterPro; IPR001037; Integrase_C.
InterPro; IPR00103708; Integrase_C.
InterPro; IPR001905; Peptidase_A2.
InterPro; IPR001905; Pept Aspartic.
InterPro; IPR001909; Retrovir_matrix.
InterPro; IPR001909; Retrovir_matrix.
InterPro; IPR000911; Retrovir_matrix.
InterPro; IPR008916; Retrov capsid_C.
InterPro; IPR008916; Retrov capsid_C.
InterPro; IPR008916; Retrov capsid_N.
InterPro; IPR0015066; Retrov capsid_N.
InterPro; IPR0015066; Retrov capsid_N.
InterPro; IPR0015066; Retrov capsid_N.
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InterPro; IPR010661; RVT_thumb.
InterPro; IPR001878; Znf_CCHC.
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Pfam; PF06815; RVT_connect; 1.

Pfam; PF06815; RVT_connect; 1.

Pfam; PF06918; zf_CGHC; 2.

PRINTS; PR00939; C2HCZNFINGER.
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PF00665; rve; 1.
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PRINTS; PR00234; HIVIMATRIX.
SMART; SM00341; ZnF_C2HC; 2.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS501141; ASP_PROTEASE; 1.
PROSITE; PS501158; ZnF_PROTEASE; 1.
PROSITE; PS501158; ZnF_PROTEASE; 1.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; 2.
AIDS; Aspartyl protease; RNA-directed DNA polymerase; Transferase; ZnC-finger.
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SEQÜENCE 1429 AA; 161586 MW; D0B9CD124DC64E19 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ح ج	781	GCGAGATCACCAAGATCGGCCCCGAGAACCCCTAC 84
۵ ۸	4 (0)	ACACCCCCGTGTTCGCCATCAAGAAGAAGACACCACCAAGTGGGGCAAGCTGGTGGC 90
۵ <		CCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 9
ם א	961	GGCCTGAAGAAGAAGAAGGGTGACCGTGCTGGACGTGGGCGACGCCTACTTC 10
۵ ۸	1021	GAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 10
۵ ۸	1081 718	ATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCAGC 11
۵ ۸	1141	
۵ د	1201 758	CGGC 12 eGly 77
۵ <	1261	CAAGATCGAGGAGCTGCGAAGCACCTGCTGCTGGGGCTTCACCACC 13
ם א	1321	HAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCC 13
۵ ۸	1381	CGAC 14 nAsp 83
۵ د	1441	PAAGCTGGTGGGCAAGCTGAACTGGGCCAGGTCTACCCCGGCATCAAGGTG 15
۵ د	1501	SACC 1
۵ <	1561	3GGC 16 3Gly 89
ه د	1621	TACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGAG 16
. د	80 1-1	CAAG 17 aLys 93
ه د	1741 938	CGCC 18 eAla 95
`	0	SAGAGCATOGTGATCTGGGGGAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGG 18
ح م	958	etGluGlyIleValIleTrpGlyLysValProLysPheArgLeuProIleGlnLysGlu 9 ccTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTC 1

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AsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLysGluGlyHisGlnMet 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; Aspartyl protesse; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protesse; RNA-directed DNA polymerase; Transferase; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 AAGGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTC
GO: 0008233; F:peptidase activity; IEA.

GO: 0004523; F:rribonuclease H activity; IEA.

GO: 00003723; F:RNA binding; IEA.

GO: 00003723; F:RNA-directed DNA polymerase activity; IEA.

GO: 00000370; F:rransferase activity; IEA.

GO: 0001670; F:rransferase activity; IEA.

GO: 0010570; F:rrinc ion binding; IEA.

GO: 0010574; P:DNA integration; IEA.

GO: 00006310; P:DNA recombination; IEA.

GO: 00006310; P:RNA-dependent DNA replication; IEA.

GO: 00106022; P:viral life cycle; IEA.
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InterPro; IPR001037; Integrase C.
InterPro; IPR0010308; Integrase C.
InterPro; IPR001909; Peptidase A2.
InterPro; IPR001969; Peptidase A2.
InterPro; IPR001969; Pepti Aspartic.
InterPro; IPR010999; Petrovir matrix.
InterPro; IPR0010919; Retrovir matrix.
InterPro; IPR008916; Retrovir matrix.
InterPro; IPR008916; Retrov Capsid C.
InterPro; IPR008919; Retrov Capsid C.
InterPro; IPR008919; Retrov Capsid C.
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PROSITE; PSS0175; ASP_PROT_RETROV; 1.
PROSITE; PSS0158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001884; Rve.
InterPro; IPR001884; Rve.
InterPro; IPR010659; RVT connect.
InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT chumb.
InterPro; IPR011878; Znf_CCHC.
Pfam; PP00607; Gag_D24; 1.
Pfam; PP00607; RnaseH; 1.
Pfam; PP00075; RnaseH; 1.
Pfam; PP00075; Rve; 1.
Pfam; PP00675; Rve; 1.
Pfam; PP00681; RVT 1; 1.
Pfam; PP06815; RVT 1; 1.
Pfam; PP06815; RVT thumb; 1.
Pfam; PP06815; RVT thumb; 1.
Pfam; PP06815; RVT thumb; 1.
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AA; 161115 MW;
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PRINTS; PRO0234; HIVIMATRIX.
SMART; SMO0343; ZNF_CZHC; 2.
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                                                                                                                           998 ValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluLysGluProIleAlaGly 1017
                                                                                                                                                                                                                    1018 ValGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysIleGlyLysAlaGly 1037
                                                                                                                                                                                                                                                                                            1038 TyrValThrAspArgGlyArgGlnLyslleValSerLeuThrGluThrThrAsnGlnLys 1057
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PubMad=14709249; DOI=10.1089/088922203771881220;

Harris M.E., Maayan S., Kim B., Zeira M., Ferrari G., Birx D.L.,

McCutchan F.E.;

"A cluster of HIV type I subtype C sequences from Ethiopia, observed
in full genome analysis, is not sustained in subgenomic regions.";

AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, Q72499; 1KGY.
GO; GO:0019012; C:virion; IEA.
GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
GO; GO:0003677; F:abNA binding; IEA.
GO; GO:0008907; F:integrase activity; IEA.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Belongs to peptidase family A2.
EMBL; A7255824; AAP76529.1; --
HSSP; Q72498; 1K6Y.
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Kim B., McCutchan F.E.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
63-JUL-2004 (TrEMBLrel. 27, Last sequence update)
63-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI TaxID=11676;
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Harris M.E., Birx D.L.;
Submitted (MAR-2003) to
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Q6X4Q6;
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778 LysileGluGluLeuArgGlyHisLeuLeuArgTrpGlyPheThrThrProAspLysLys 79 1333 CACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACC 13	1393 GTGCAGCCCATCGAGCTGCCCGAGAAGCAGGACCGTGAACGACATCCAGAAGCTG 145:	1513 AAGCTGCTGCGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAG 1	1573 CTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGAC 1	1633 CCCAGCAAGGACCTGGTGGCCGACATCCACAAGCAGGGCCCACGACCACGACCTGCCAG 16 	1693 ATCTACCAGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGC 1	1753 CACACCAACGAGGAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATC 1 	3 GTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACC 1 	TGGTGAACCGACTACTGGCAGGCCACCTGGATCCCGAGTGGGAGTTGGTGAACACCCCC 	CCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGACCCATCATCGGGGCCGAGACCTTC 1	TACGTGGACGGCCGCCACCGCGACACACATCGGCAGGCCGGCTACGTCACCGAC 	3 CGGGGCCGGCAGAAGATCGTGACCTGACCGAGACCACCAGAAGACCGACTGCAG 	GCCATCCAGCTGGCCGCGCAGCAGCGAGCTGAACATCGTGACCGACAGCAG :::	3 TACGCCTGGGCATCATCCAGGCCCAGCCCGACAAGAGCGAGGCGAGCTGGTGAACCAG	2233 ATCATCGAGCACTGATCAAGAAGAGAGAGGTGTACCTGAGGTGGCTGGGTGCCGCCCACAAG 	2293 GGCATCGGCGCAACGAGCAGATCGACAAGCTGGTGAGGCATCCGCAAGGTGCTG 2352	2353 TTCCTGGACGCATCGAT 2370
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-y 437 -y 437 -g 312 457	w 4 4	.e 497 .c 492 	ic 552 x 537	C 612 	C 672 	.G 732 	IG 792	G 852 637	'G 912 	G 972 - 10 677	'G 1032 	C 1092			1	
	CAGGTGCGCGCGCACCCCCGCGGCGGCGGCGCCGGCGCCGGGGCCCCCTGAAC	PheProGlnIleThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlyGlnIle AAGGAGGCCCTGCTGGACACCGGCGCCGACGACGTGCTGGAGAGATGAGCCTGCCC :::	GGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTAC	GACCAGATCCTGATCGAGATCTGCGGCAAAGAGCCATCGGCACCGTGCTGATCGGCCCC	ACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTC	CCATCAGCCCCATCGAGACCGTGCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAG 	GTGAAGCAGTGGCCCCTGACCGAGGAGAACATCAAGGCCCTGACCGCCATCTGCGAGGG 	793 ATGGAGAAGGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTG 	TTGGCCATCAAGAAGAAGACAGCACCAAGTGGCGGAAGCTGGTGGACTTCCGGGAGCTG 	AACAAGGGCACCCGGGACTTCTGGGAGGGGGGGGGGTGGGGATCCCCCACCCCGCCGGCCTG 	973 AAGAAGAAGAAAGGGTGACCGTGCTGGACGTGGGGCGACGCCTACTTCAGCGTGCCCCTG 	GACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCC	GGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGGTGGAAGGGCAGCCCCAGCATCTTC	CAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATC 	CAGCACCGCGCC	CCCCGACAAGAAG
	CCGAGCGCCA(CGAGCGCCA) algluargglr GCATCAAGGT(erlleLysVal TGCTGGAGGAC alLeuGluGlu	GCTTCATCAAC JyPheIleLye	TCGGCACCGTC eGlyThrVal	AGCTGGGCTGC 	AGCCCGGCATC ysProGlyMet	CCCTGACCGCC 	AGAACCCTAC	AGCTGGTGGAC ysLeuvalAsp	GCATCCCCCAC 	ACGCCTACTTC spAlaTyrPhe	CCAGCATCAAC	GGAAGGGCAGC rpLysGlySer	CCCGCAACCCC ::: aGlnAsnPrc	TACCAGTACATGGACGACCTGTACGTGGGCGACCTGGAGATCGGCCAGCA 	ANGALCGAGGAGCTGCCCAAGCCTGCTGCGCCTTCACCACCCCCCGA
	::: :::: ::ysThrGlyv	ProLeuvals :GACGACACCG AspAspThrv	GGCATCGCCG 	AAGAAGGCCA 'LyslysAlaI	ATGCTGACCC 	GTGAAGCTGA VallysLeuL	AAGATCAAGG	ATCGGCCCG	AAGTGGCGCA LystrpArgl	GTGCAGCTGG ValGlnLeuG	GACGTGGGCG AspvalGlyA	TTCACCATCC	CCCCAGGGCT ProGlnGlyT	CCCTTCCGCG ProPheArgA	GGCAGCGACC	crececrese
	CCCCCCAGC	uTrpGlnArg .CACCGGCGCC pThrGlyAla	GATGATCGGC	GATCTGCGGC ulleCysGly	CGGCCGCAAC eGlyArgAsn	GACCGTGCCC uThrValPro	GACCGAGGAG uThrGluGlu	GATCACCAAG sileThrLys	GGACAGCACC BASDSerThr	CTTCTGGGAG pPheTrpGlu	GACCGTGCTG 	GTACACCGCC 8TyrThrAla	CAACGTGCTG	GATCCTGGAG : glleLeuGlu	CCTGTACGTG 	CAAGCACCTG
	3CGGCGACAA ::: rgArgasnas AGATCACCT	InileThrLe CCCTGCTGGA aLeuLeuAs	GAAGCCCAA	rccrgarcga eLeuIleGl	rgaacarcar alasnileil	GCCCATCGA erProlleGl	AGTGGCCCCT nTrpProLe	AGGAGGGCAA /8GluGlyLy	rcaagaagaa elyslysly	SCACCCAGGA	AGAAGAGCGT /8LysServa	ACTTCCGCAA	SCTACCAGTA	SCATGACCAA :: srMetThrar	ACATGGACGA	AGGAGCTGCG
418 LysAspC 253 AAGGCCC ::: 438 GluAlaA		478 PheProG 433 AAGGAGG ::: 498 ArgGluA	493 GGCAAGTC 518 GlyLysT	553 GACCAGA: 538 AspGlnI	613 ACCCCCG7 558 ThrProve	673 CCCATCAC 578 ProlleSe	733 GTGAAGC 598 VallysG	93 ATGGAGA 18 MetGluLy	853 TTCGCCA7 638 PheAlaI	913 AACAAGCC 658 AsnLysa	73 AAGAAGA. 78 LysLysLy	033 GACGAGG/ 698 AspGluSe			1213 TACCAGT 758 TyrglnTy	73 AAGATCG
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                                                                                                                                                                      MEDLINE=99214383; PubMed=10196340; MEDLINE=99214383; PubMed=10196340; MeDLINE=99214383; PubMed=10196340; Movitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.; Molecular cloning and phylogenetic analysis of human immunodeficiency virus type I subtype C: a set of 23 full-length clones from Botswana..; M. Virol. 73:442-4427(1999).
-! SIMILARITY Belongs to peptidase family A2. EMBL, AFI10976; ABOING to peptidase family A2.
                                                                                                                                                                                                                                                                                                                                           R GO; GO:0019012; C:virion; IEA.

GO; GO:00041901; F:aspartic-type endopeptidase activity; IEA.

GO; GO:000817; F:DNA binding; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008235; F:peptidase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005109; F:inic ion binding; IEA.

GO; GO:0006210; F:inic ion binding; IEA.

GO; GO:0006210; F:inic ion binding; IEA.

GO; GO:0006210; P:DNA integration; IEA.

GO; GO:0006218; P:PNRA-dependent DNA replication; IEA.

GO; GO:0006218; P:PNRA-dependent DNA replication; IEA.
                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein
Human immunodeficiency virus 1.
                                                                                                                              Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
                               1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000721; Gag p24.
InterPro; IPR001037; Integrase C.
InterPro; IPR001037; Integrase C.
InterPro; IPR0010309; Integrase C.
InterPro; IPR0010909; Peptidase A2.
InterPro; IPR001909; Peptidase A2.
InterPro; IPR001909; Retrovirmatrix.
InterPro; IPR001091; Retrovirmatrix.
InterPro; IPR001091; Retrovirmatrix.
InterPro; IPR001091; Retrovirmatrix.
InterPro; IPR0010819; Retrovirmatrix.
InterPro; IPR0010819; Retrovirmatrix.
InterPro; IPR0010819; RVT.
InterPro; IPR0010819; RVT.
InterPro; IPR010878; RVT.
InterPro; IPR010878; RVT.
InterPro; IPR010871; RVT.
InterPro; IPR010871; RVT.
InterPro; IPR010871; I.
Pfam; PP00507; Gag_p24; I.
Pfam; PP00007; RABSEH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00343; ZnF C2HC; 2.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZP_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00077; RVP; 1.
Pfam; PF00078; RVT 1; 1.
Pfam; PF06815; RVT connect; 1.
Pfam; PF06817; RVT chumb; 1.
Pfam; PF00098; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SM00343; ZF_C2HC; 2.
                               PRELIMINARY;
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RESULT 7
Q9WF96
ID Q9WF96
AC Q9WF96;
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                                                                                                                                                                                                                       72
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc; Zinc-finger.
SEQUENCE 1427 AA; 160518 MW; FBDA73D603A68B18 CRC64;
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                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                        1.26e-151
3986.00
97.58%
93.38%
86.97%
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420 498 480 600

558

540 538 999 578 720

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AGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1080
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                                CAGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGCCGAGCGC
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GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:000510; P:DNA integration; IEA.

GO; GO:000510; P:DNA recombination; IEA.

GO; GO:0005210; P:DNA recombination; IEA.

BR GO; GO:0005210; P:PNA recombination; IEA.

BR GO; GO:0005210; P:PNA-dependent DNA replication; IEA.

BR GO; GO:0005210; P:Viral life cycle; IEA.

GO; GO:0005210; P:Viral life cycle; IEA.

BR InterPro; IPR001037; Integrase_Zn_N.

BR InterPro; IPR001039; Peptidage_AZ.

BR InterPro; IPR001099; Peptidage_AZ.

BR InterPro; IPR001099; Peptidage_AZ.

BR InterPro; IPR001099; Peptidage_AZ.

BR InterPro; IPR001099; Retrov_cappid_C.

BR InterPro; IPR001099; Retrov_cappid_C.

BR InterPro; IPR001099; Retrov_cappid_C.

BR InterPro; IPR001099; Retrov_cappid_C.

BR InterPro; IPR001099; Retrov_cappid_N.

BR Fdam; PP00047; Rayer i.

BR Fdam; PP00076; Rayer i.

BR Fdam; PP00078; Rayer i.

BR Pfam; PP00078; Ray
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Matches:
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Mismatches:
Indels:
Gaps:
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SEQUENCE 1430 AA; 161540 MW;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pfam; PF00607; Gag p24; I.
Pfam; PF02022; Integrase Zn; I.
Pfam; PF00075; RnaseH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00078; RVT_1; 1.
Pfam; PF06813; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00098; zf-CCHC; 2.
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InterPro; IPR000477; RVTB(
InterPro; IPR010659; RVT_
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Pfam; PF00075; R
Pfam; PF00665; r
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Pfam; PF00078;
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                                                                                                           GAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGGAGCCCGTGCACGGC 1620
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                                                                                                                                                                                                                                    939 ArgArgThrAlaHisThrAsnAspValLysGlnLeuThrGluAlaValGlnLysIleAla 958
                                                                                                                                                                                                                                                                         839 IleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIleTyrProGlyIleLysVal
                                                                                  GluGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGluProValHisGly
                                    ATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTG
                                                                        CGCCAGCTGTGCAAGCTGCTGCGCGCGCCCAAGGCCCTGACCGACATCGTGCCCCTGACC
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01-NOV-1999 (TrEMBLrel. 12, Created)
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
J. Virol. 73:4427-4432(1999). SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS00141, ASP_PROTRARS; 1.
PROSITE; PS50175; ASP_PROT RETROV; 1.
PROSITE; PS50188; ZF_CCHC; Z.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc; Zinc-finger. SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.; MSSP; 070622; 1HVN.

GO; GO:001910; C:virion; IER.

GO; GO:001910; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0008233; F:DNA binding; IEA.

GO; GO:0008233; F:RDA binding; IEA.

GO; GO:0008233; F:RDA binding; IEA.

GO; GO:0003864; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003864; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003864; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0001896; F:RTANG-directed DNA polymerase activity; IEA.

GO; GO:0016740; F:Tansferase activity; IEA.

GO; GO:0016010; F:Tansferase activity; IEA.

GO; G 1427 AA; 161326 MW; B9FC43C29B26CFA2 CRC64 Gag-pol polyprotein.

Human immunodeficiency virus 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus

NCBL TaxID=11676; -!- SIMILARITY: Belongs to peptidase family A2. EMBL; AF110964; AAD17047.1; -. HSSP; Q70622; 1HVN. InterPro; IPR000477; RVTse. InterPro; IRR010659; WT connect. InterPro; IPR010661; RVT_thumb. InterPro; IPR001878; Znf_CCHC.

Alignment Scores:

973 AAGAAGAAGAGGGGGCCGGCCGGGCGACGCCTACTTCAGCGTGCCCCTG 1032	1153 CAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCACCCCCGAGATCGTGATC 1212	1273 AAGATCGAGGAGCTGCCAAGCACCTGCTGCGGCTTCACCACCCCCGACAAGAAG 1332		AAGCTGCTGCGGGGGGCGCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAG 15	1633 CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAG 1692	1753 CACACCAACGACGAGACTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATC 1812	1873 TGGTGGACCGACTGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCC 1932
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ed. No.: ore: rcent Sim Bt Local ery Match : -09-610-3	AGGCCCCAAGCGCATCATCAACTGCTAACTGCCGCAAGGGCCACTGCCCGC 13 AAGGCCCCAAGCGCATCATCAACTGCTAACTGCGCAAGGGCCAATGCCCCGC 13 Ly6G1yPtCATGATG1leValLy8Cy8PheAanCy8G1yLy8G1uG1yH18IleAlaArg 39 AACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGACCACCACAGT 19	400 ABNCYSATGALGAFGLYSIYSGLYCYSTTPLYSCYSGLYLYSGLUGLYHISGLNMEt 41 193 AAGGACTGCACCGAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGC 25		nii GCC GTA	Infyr 53 3CCCC 61 yPro 55 ACTTC 67	560 ThrProlleAsnileileGlyArgAsnMetLeuThrGlnLeuGlyCysThrLeuAsnPhe 57 673 CCCATCAGCCCATCGAGACCGTGCCGTGAAGCTGAAGCCCGCATGACGCCCCAAG 73 [Db 600 VallysGlnTrpProLeuThrGluGluLysIleLysAlaLeuThrAlaileCysGluGlu

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Property Process, Transfer, 1.

Ream; Procoffs; Trust. 1.

Ream; Procoffs; RVP; 1.

Ream; Procoffs; RVT_connect; 1.

Ream; Procoffs; RVT_connected; RVT_CONN
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                                                                                       InterPro; IPR010659; RVT connect
InterPro; IPR010661; RVT thumb.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                   Pfam; PP00540; Gag_pl7; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; RnaseH; 1.
                           RNaseH.
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Wholecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Bt Stewand.;

Virus type 1 subtype C: a set of 23 full-length clones from Bt Stewand.;

J. Virol. 73:4427-4432(1999)

C. -- SIMILARITY: Belongs to peptidase family A2.

EXBL, API10978; AAD17162.1; -- SIMILARITY: Belongs to peptidase family A2.

EXBL, API10978; AAD17162.1; -- SIMILARITY: Belongs to peptidase activity; IEA.

GO; GO:00019012; C:virion; IEA.

GO; GO:00019012; C:virion; IEA.

GO; GO:00019012; F:nbonuclease activity; IEA.

GO; GO:0001373; F:nbonuclease H activity; IEA.

GO; GO:0001373; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0001964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0001964; F:rinc ion binding; IEA.

GO; GO:0005109; F:rinc ion binding; IEA.

GO; GO:0005109; F:rinc ion binding; IEA.

GO; GO:0006210; P:proteolysts and peptidolysis; IEA.

GO; GO:0006210; P:DNA integration; IEA.

GO; GO:0006210; P:NNA-dependent DNA replication; IEA.

GO; GO:0006219; P:RNA-dependent DNA replication; IEA.

RO; GO:0006210; P:RNA-dependent DNA replication; IEA.

RO; GO:0006210; P:RNA-dependent DNA replication; IEA.

RO; GO:0006210; P:RNA-dependent DNA replication; IEA.
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GGCATCGCCGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG
                                                                    GCCATCCAGCTGGCCCTGCAGGACAGCGGCAGGTGAACATCGTGACCGACAGCCAG
                                                                                                                                                                                                                                            MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Wontano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL TAXID=11676;
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InterPro; IPR010969; Pept_Asp_AS.
InterPro; IPR010999; Retrovir_matrix.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR008916; Retrov_capsid_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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J. Virol. 73:4427-4432(1999).
                                                                                                                                                                                                                    1120 GlyIleGlyGlyHisGluGlnValAspLysLeuValSerSerGlyIleArgLysValLeu
                                      ATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCC
                                                     CACACCAACGACGTGAAGCAGCTGACGAGGCCGTGCAGAAGATCGCCATGGAGGAGCATC
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SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannbe Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink I Essex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9WF65 PRELIMINARY; PRT; 1427 AA. Q9WF65; Cluvov-1999 (TrEMBLrel. 12, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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BRBL; AR110952; AAD17030.1; -

BRBL; AR110952; AAD17030.1; -

BRSP; Q70622; IHVN.

GO; GO:001910; F:aspartic-type endopeptidase activity; IEA.

GO; GO:000357; F:INRA binding; IEA.

GO; GO:000357; F:INRA binding; IEA.

RO; GO:000423; F:RNA binding; IEA.

RO; GO:000423; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000423; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000523; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000523; F:RNA-directed DNA polymerase activity; IEA.

RO; GO:000523; F:RNA-directed DNA polymerase activity; IEA.

RO; GO:000520; F:III and ferase activity; IEA.

RICEPPO: IPRO0007; Fept Aspartic.

RICEPPO: IRRO00905; Retrovic_matrix.

RICEPPO: IRRO00905; Retrovic_matrix.

RICEPPO: IRRO00905; Retrovic_matrix.

RICEPPO: IRRO00905; RAT connect.

RICEPPO: IRRO00605; RYT connect.

RICEPPO: IRRO00605; RAT CONNECT.
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                           BREADLY, TAILLY.

BR GOS GO:0019012; C:virion; IEA.

BR GOS GO:00019012; C:virion; IEA.

BR GOS GO:00019012; C:virion; IEA.

BR GOS GO:00019012; F:sapartic-type endopeptidase activity; IEA.

BR GOS GO:0001907; F:integrase activity; IEA.

BR GOS GO:0001907; F:integrase activity; IEA.

BR GOS GO:0001907; F:integrase activity; IEA.

BR GOS GO:0001907; F:RNA binding; IEA.

BR GOS GO:0001908; F:RNA binding; IEA.

BR GOS GO:0001909; F:RNA dependent DNA reptically Sis; IEA.

BR GOS GO:0001909; F:RNA dependent DNA reptication; IEA.

BR GOS GO:000101019; F:RNA dependent DNA reptication; IEA.

BR INTERPRO: IPR001037; Integrase Zn N.

BR INTERPRO: IPR001099; Retrovir_D17.

BR INTERPRO: IPR001099; Retrovir_D17.

BR INTERPRO: IPR001099; Retrovir_matrix.

BR INTERPRO: IPR001099; Retrovir_matrix.
                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein.
Human immunodeficiency virus 1.
                                                                                                                                                                                                 Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 73:4427-4432(1999).
-!- SIMILARITY: Belongs to peptidase family A2.
EMBL; AF110967; AAD17072.1; -.
                                                                                              PRT; 1437 AA
2353 ITCCTGGACGCCATCGAT 2370
                Pfam; PF00665; rve; 1.
Pfam; PF00077; RVP; 1.
Pfam; PF00078; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF06939; C2PCZNF1NGER.
PRINTS; PR00234; H1VIMATERIX.
SMART; SM0343; ZNF_CZHC; 2.
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                                                                                            PRELIMINARY;
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                  AAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACCCCCCGACAAGAAG 1332
                                                                                CACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACC 1392
                                                                                                                                                GTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTG 1452
                                                                                                                                                                                                              GTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGC 1512
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                       Zinc;
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PROSITE; PS50175; ASP_ROTT RETROV; 1.
PROSITE; PS50159; ZF_CHC; 2.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc-finger.
SEQUENCE 1437 AA; 161978 MW; 65DAA2562FC317A6 CRC64;
                                                    1437
740
30
116
10
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              US-09-610-313B-30 (1-2469) x Q9WF77
                                                    8.67e-151
3965.00
96.73*
92.96*
86.52*
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AAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAG GlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSerThrLys CAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAGAGAAAAAGAGAGCGTGCTGCTGGAC AGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTG CGCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATG GGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCCATCGAGCTGCCCGAGAAGGAG ACCGGCAAGTACGCCAAGATGCGCACCGCCCACAACGACGTGAAGCAGCTGACCGAG CTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGG TGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTG TTCCGCGCCCCGCAACCCCCGAGATCGTGATCTACCAGTACATGGACGACGTGTACGTGGGC TACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGGCGCGCCCAAGGCCCTGACC GACATCGTGCCCCTGACCGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTG GCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGC ờ, A ở 8 6 g g & g 8 6 8 6 8 6 8 6 \$ B \$ B \$ B \$ 셤 ठ 8 6 8 6 8 8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO034; CZHCZNFINGER.
PRINTS; PRO034; HIVHATRIX.
SMART; SM00343; ZnF_CZHC; 2.
PROSITE; PS00141; ASP_PROTRETROV; 1.
PROSITE; PS50175; ASP_PROTRETROV; 1.
PROSITE; PS50178; ZnF_CCHC; 2.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
POLYPOTOTEIN; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ATGGCCGAGGCCATGAGCCAGGCCACCACCCCAACATCCTGATGCAGCGCAGCAACTTC
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Gag_p24.
Integrase_C.
Integrase_Zn N.
Peptidase_A2.
Pept Aspartic.
Pept Aspartic.
Pept Aspartic.
                                                                                                                                                                                   Retrovir_p17.
Retrov_capsid_C.
Retrov_capsid_N.
RNaseH.
                                                                                                                                                                                                                                                                                                                 InterPro; IPR000477; RVTse.
InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT humb.
InterPro; IPR01878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00607; Gag_P24; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; RnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; RVP; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_chumb; 1.
Pfam; PF06817; RVT_chumb; 1.
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97.33%
92.62%
86.35%
                        InterPro; IPR001037; II
InterPro; IPR001998; II
InterPro; IPR001998; II
InterPro; IPR001969; Pe
InterPro; IPR0101969; Re
InterPro; IPR010199; Re
InterPro; IPR0010919; Re
InterPro; IPR001919; Re
InterPro; IPR001919; Re
InterPro; IPR001919; Re
InterPro; IPR001919; Re
InterPro; IPR001916; Re
InterPro; IPR001916; Re
InterPro; IPR001916; Re
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Best Local Similarity:
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                                SerGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnPro 1099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                                                                                                                                                                                                                                                                                                                 GluThrThrAsnGlnLysThrGluLeuGlnAlaIleGlnLeuAlaLeuGlnAspSerGly
                                                                                                                                                                                                               AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACC
                                                                                                          AAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACC
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GO, GO:001919; C:virion; IEA.

GO, GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO, GO:0003197; F:DNA binding; IEA.

GO, GO:0008233; F:peptidase activity; IEA.

GO, GO:0008233; F:peptidase activity; IEA.

GO, GO:0003723; F:ribonuclease H activity; IEA.

GO, GO:0003723; F:RNA binding; IEA.

GO, GO:0003783; F:RNA-directed DNA polymerase activity; IEA.

GO, GO:0005198; F:structural molecule activity; IEA.

GO, GO:000574; F:zinc ion binding; IEA.

GO, GO:000574; P:zinc ion binding; IEA.

GO, GO:0006574; P:zinc ion binding; IEA.

GO, GO:0006578; P:zinc ion binding; IEA.
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MEDLINE=99214383; PubMed=10196340;
Novitesky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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-!- SIMILARITY: Belongs to peptidase family A2.
EMBL, AFIL10965, AAD17056.1; -.
HSSP, Q70622; 1HVN.
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1513 AAGCTGCTGCGCGCCCCCCCCCCCCCCCCCCCCCCCCCC	ADXS QBADXS QBADXS QBADXS QBADXS O1-WAR-2003 (TEWBLrel. 23, Las O1-WAR-2004 (TEWBLrel. 23, Las O1-WAR-2004 (TEWBLrel. 26, Las Gag-pol fusion polyprotein (Fra Name-gag-pol, Human immunodeficiency virus 1. Viruses; Retroid viruses; Retro
480 PhebrodinileThirLeuTrpGlinkrgProLeuValSerIleLygValGlyGlnIle 499 433 AAGGAGGCCTGCTGGACCCGGCGCCGACCCTGCTGGAGGACTGCCCCCCCC	780 iysiledludludarggiudisledledlysfrpdiyleuthritheroksplys199 1333 CACCAGAAGGAGCCCCCTTCCTGTGGATGGCTACGAGCTGCACCCCGACAAGTGGAC 1392

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              MEDLINE-22775625; PubMed=12487816; DOI=10.1089/088922202320886325; MEDLINE-22775625; PubMed=12487816; DOI=10.1089/088922202320886325; Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B., Kigozi G., Kiwanuka N., Phillips J.B., Mechen M., Lutalo T., Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L., McOutchan F.E., McCutchan F.E., Mamong 46 near full length HIV type 1 genome sequences from Rakai District, Uganda, subtype D and AD recombinants predominate.";
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GO, GO:001901; C:virion; IEA.

GO, GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO, GO:000317; F:DNA binding; IEA.

GO, GO:0008233; F:peptidase activity; IEA.

GO, GO:0008233; F:peptidase activity; IEA.

GO, GO:0003723; F:RNA binding; IEA.

GO, GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO, GO:000198; F:structural molecule activity; IEA.

GO, GO:0015074; F:RNA-directed DNA polymerase activity; IEA.

GO, GO:0015074; F:Rna-directed DNA polymerase activity; IEA.

GO, GO:0015074; F:DNA integration; IEA.

GO, GO:0006508; P:DNA integration; IEA.

GO, GO:0006508; P:Proteolysis and peptidolysis; IEA.

GO, GO:0006508; P:Viral life cycle; IEA.
                                                                                                                                                                                                                                                                                                                         Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to peptidase family A2.
--- EMBL; AF48491; ANV33556.1; ---
HSSP; P24736; INCP.
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             Robb M.L.;
the EMBL/GenBank/DDBJ databases
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GO. 0003677; F. 101 Equase activity. I.

GO. GO. 0008231; F. 101 Equase activity. I.

GO. GO. 0004523; F. 100 Equase activity. I.

GO. GO. 0003723; F. 100 Equase activity. I.

GO. GO. 0003723; F. 100 Equase activity. I.

GO. GO. 0003723; F. 100 Equase activity. I.

GO. GO. 0005108; F. 100 Equase activity. I.

GO. GO. 0006310; P. 100 Equase activity. I.

GO. GO. 0006310; P. 100 Equase activity. I.

GO. GO. 0006310; P. 100 Equase activity. I.

GO. GO. 0006278; P. 100 Equase activity. I.

GO. GO. 0006310; P. 100 Equase activity. InterPro: IPRO01995; Peptidase A. I.

InterPro: IPRO01995; Peptidase A. InterPro: IPRO01999; Retrovir matrix. InterPro: IPRO01999; Retrovir matrix. InterPro: IPRO01999; Retrovir matrix. InterPro: IPRO01999; Retrovir matrix. InterPro: IPRO01999; Retrovic appsid. C. InterPro: IPRO01999; Retrovic appsid. Inter
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InterPro; IPR010661; RVT_thumb.
InterPro; IPR001878; Znf_CCHC.
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PF06815; RVT connect; 1.
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PF00075; RnaseH; 1-
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Harris M.E., Birx D.L.,
Submitted (FEB-2002) to
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Pfam; PF06817; RVT thumb; 1.

Pfam; PF00098; zf-CCHC; 2.

SMART; SM00134; ASP-CFCHC; 2.

PROSITE; PS010141; ASP-PROTEASE; 1.

PROSITE; PS50175; ASP-PROTEASE; 1.

PROSITE; PS50158; ZF CCHC; 2.

AIDS; Aspartyl protease; Core protein; Hydrolase; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase.

NON_TER
                                                                                                                                              SEQUENCE 1427 AA; 161058 MW; 20559041E2A88B5C CRC64;
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793 ATGGAGAGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTG 852	TTGGCCATCAAGAAGAGACAGCACCAAGTGGGGCAAGCTGGTGGACTTCCGGGAGGTG	AACAAGGCACCCCAGGACTTCTCGGAAGTGCAGCTGGCATCCCCCCCC	AAGAAGAAGAGGGGGGCGGGCGGGGGGGGGGGGGGGGG	1033 GACGAGGACTTCCGCCAGCTCCACCCCCCCCGCATCAACAACGAGACCCCC 1092 	1093 GGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCCCCAGCATCTTC 1152 	CAGAGCAGCATGACCAGATCCTGGAGCCCTTCCGCCCCCCAGACCCCCGAGATCGTGATC	TACCAGTACATGGACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACC 	AAGATCGAGGAGCTGCGCAAGCACCTGCTGCGGCTGGGGCTTCACCACCCCCGACA 	1333 CACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCCCCCGACAAGTGGACC 1392 	1393 GTGCAGCCCATCGAGCTGCCCGAGAAGAGAGAGCTGGACCGTGAACGACATCCAGAAGCTG 1452 	1453 GTGGGCAAGCTGAACTGGGCCAGATCTACCCCGGCATCAAGGTGGGCAGCTGTGC 1512	1513 AAGCTGCTGCGCGCGCAAGGCCCTGACCGACTCGTGCCCCTGACCGAGGAGGCCGAG 1572	1573 CTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACGAC 1632	1633 CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGGACCTGCAG 1692	1693 ATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACGCC 1752	1753 CACACCAACGACGCAGACGCCGAGGCCGTGCAGAACATCGCCATGGAGGCATC 1812 	1813 GTGATCTGGGGCAAGACCCCCAAGTTCCGCCCATCCAGAAGGAGACCTGGGAGACC 1872 :::	1873 TGGTGGACCGACTACTGGCGAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCC 1932

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GO; GO:0006278; P:RNA-dependent DNA repl

GO; GO:0016032; P:viral life cycle; IEA,

InterPro; IPR001037; Integrase C.

InterPro; IPR001037; Integrase Zn. N.

InterPro; IPR001995; Peptidase A2.

InterPro; IPR001995; Retrovir_pl7.

InterPro; IPR001965; RNASH.

InterPro; IPR0010659; RNT_connect.

InterPro; IPR010659; RNT_connect.

InterPro; IPR010659; RNT_connect.

InterPro; IPR010659; RNT_connect.

InterPro; IPR01067; RNT_connect.

Pfam; PF00077; RNP; I.

Pfam; PF00077; RNP; I.

Pfam; PF00077; RNP; I.

Pfam; PF00079; RNP; I.

Pfam; PF000195; RNPT_connect; I.

Pfam; PF000195; RNPT_connect; I.

Pfam; PF000399; CCHCZNINGER.

PRINTS; PR00234; HIVIMARTIX.

SWART; SN00349; ZnF CCHC; I.

PROSITE; PS0115; ASP PROTEASE; I.

PROSITE; PS0115; ASP PROTEASE; I.
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A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-1002 <THE>
A;Cross-references: UNIPROT:P12499; EMBL:M22639; NID:g329377; PIDN:AAA45366.1; PID:g3293
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-701-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54378
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Reference number: S54377
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GNLJG3
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S23820
GNLJFP
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-MODEL=frame+ nzp.model -DBV=xlh
-Q=/Cgn2 1/USPTO spool/US09610313/runat_31052005_155137_15159/app_query.fasta_1.7893
-Q=/Cgn2 1/USPTO spool/US09610313/runat_31052005_155137_15159/app_query.fasta_1.7893
-DB-PIR 79 -QFWT=fastan -SUPFIX=nzp.rpr -MINNATCH=0.1 -LOOPCL=0 -LCOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UOCALIGN=200 -THR.SCORE=pct -THR MAX=100 -TRH MIN-0 -ALIGH=15 -MODE=LOCAL
-OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=US09610313 @CGN 1 1_189 @runat_31052005_155137_15159 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAAT -DSPSBLOKE=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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pol polyprocein -
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(c) 1993 - 2005 Compugen Ltd.
                                                                                                                   - protein search, using frame plus n2p model
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Database

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117 TGCCAGACCCCCCTGGTAGCATCAAGTTGGCCGGCCCAGATCAAGACCCCTGGGAC 450 6.1 TrgGlinty [11] [11] [11] [11] [11] [11] [11] [11	Qy 1471 GCCAGCCAGATCTACCCCGGCATCAAGCTGCCAGCTGCTGCTGCGCGCGC	Qy 1531 AAGGCCCTGACGACATCGTGCCCCTGACCGAGGGCCGAGGAGCTGGCCGAGAAC 1590	Qy 1591 CGCGAGATCCTGCGCGAGCCCTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTG 1650 	GCCGAGATCCAGAAGCAGGCCACGACCACGACCTACCAGATCTACCAGGAGCCCTTC 171	<pre>Qy 1711 AAGAACTGAAGACCGGCCAAGATGCGCACGCCCACCACCACGACGTGAAG 1770</pre>	1771 CAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGGCATCGTGATCTGGGGCAAGACC 183 [1831 CCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGGTG	195 580	TACCAGCTGGAGAAGGAGCCCATCATCGGCGCGAGACCTTCTACGTGGACGGCCCGCC	2011 AACCGCGAGACCAAGATCGCCAAGGCCGGCTACGTCACCGACGGGGCCGGCACAAAGATC	213	Qy 2131 CAGGACAGCGGGGGGGGGGGGGGCGGCGGGCGGGCGGGGGG	Oy 2191 CAGGCCCAGCCAGAGAGAGAGAGAGAGAGAGAACCAGATCATGAGAGAGA	2 6		RESULT 2 GNLJND HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate NDK) N;Contains: endonuclease (EC 3.1); retropepsin (EC 3.4.23.16); RNA-directed DNA polym C;Species: human immunodeficiency virus type 1, HIV-1	A;Note: host Homo sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004 C;Accession: JQ0067 R;Shire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A	Gene 81, 275-284, 1989 A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunoc A;Reference number: JQ0065; MUID:90034200; PMID:2806917 A;Accession: JQ0067
	TGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC 45	61 TrpGlnArgProLeuValThrIleLy811eG1yG1yG1nLeuLy8G1uAlaLeuLeuAsp 51 ACCGGCGCCGACGACACCGTGCTGGAGAGAGAGACCCGGCAGAGAGAG	ThrGlyAlaAspAspThrValLeuGluGluMetAsnLeubroGlyLySlTxpLySPFoLyS 10 ATGATGGGGGCATGGGGGGCTTCATCAAGGTGGGCGCAGTACGACCAGATCCTGATGGG 57 L	MECIIECIYGIYIIECIYGIYTHETIELYSVALARIGGINIYIABDOLNILECHULIECIU 12 ATCTGCGCCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCCCCC	GGCCGCAACGTGACCCGGCTGGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGCTGCACGAGCGTGCACCATCGAGCTGCAACGAGCATCCCCATCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	ACCTGCCCGTGAAGCTGAAGCCCGGACGCCCCCAAGGTGAAGCAGTGGCCCTG	ACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGGAGGAGAGGAGGAGAGGGCAAG	ATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCGTGTTCGCCATCAAGAAG 87 :::::::	GACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTTTTTTT	TTCTGGGAGGTGCAGCTGGGCATCCCCCACCGGCCTGAAGAAGAAGAAGGAGGTGTG	91 ACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGACGACGACGACGACACTTCCGCAAG	1 TACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTAC 1111	1 APINITATE RECONSTITUTE PROPERTY OF THE PROPE	ARCTIGAGECCTTCCGCGCCCGCAACCCCGAGATCGTGATTACCAGTACATGGACGC 123 ATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATTACCAGTACATGGACGAC 123 ATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATTACCAGTACATGGACGAC 123 ATCCTGGAGCCCTTCCGCGCCCAACCGAGATCGAGATCGAGATCAACAGAACAGACAACAGAACAACAACAACAACAACAACA	CTGTACGTGGGCACCTGGAGATCGGCACGCACCACCACAATCGAGGAGCTGCGC 129	1 AAGCACCTGCTGCGCTGCGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCC 135:::	51 TTCCTGTGGATGGGCTACGAGCTGCACCGCGACAGTGGACCGTGGAGCCCATCGAGCTG 141.	1 CCCGAGAAGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGG 147

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psin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate NDK) ndonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polyman immunodeficiency virus type 1, HIV-1 Homo sapiens (man) (man) 9-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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                                    CCCGAGAAGGAGACCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGG
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A; Molecule type: DNA
A; Residues: 1-1002 <SP1>
A; Residues: 1-1002 <SP1>
A; Cross-references: UNIPROT: P18802; GB: M27323; NID: g328154; PIDN: AAA44869.1; PID: g328158
C; Comment: Specific enzymatic cleavages may yield mature proteins including protease, re C; Genetics:
C; Genetics: A; Gene: pol
C; Superfamily: pol polyprotein
C; Superfamily: pol polyprotein
C; Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nuclec
F; 56-154/Product: retropepsin #status predicted <RTP>
F; 80/Active site: Asp (shared with dimeric partner) #status predicted
                                                                                                                                                                                       TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAG 279
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	REBULT 3 GOWNLY HIV-1 retropopain (EC 3.4.23.16) - human immunodeficiency virus type i (isolate LAV-la) HIV-1 retropopain (EC 3.4.23.16) - human immunodeficiency virus type i (isolate LAV-la) HIV-1 retropopain (EC 3.4.23.16) - human immunodeficiency virus type I, HIV-1 HIV-1 retropopain (EC 3.4.23.16) - human immunodeficiency virus type I, HIV-1 HIV-1 retropopain (Ball A) HIV-1 retrop

a & a	461 AsnArgGluIleLeuLysGluProValHisGlyValTyrTyrAspProSerLysAspLeu 480 1648 GTGGCCGAGATCCAGAAGGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGAGACCC 1707 :::	A;Gene: pol C;Superfamily: pol p C;Keywords: AIDS; as F;69-167/Product: re F;93/Active site: As	A;Gene: pol C;Superfamily: pol polyprotein C;Keyworda: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo P;69-167/Product: retropepsin #status predicted <rtp> F;93/Active site: Asp (shared with dimeric partner) #status experimental</rtp>
S a	1708 TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGGTGCGCACGCCCACACGACGACGG 1767 	Alignment Scores: Pred. No.: Score:	1.94e-154 Length: 1015 3513.00 Matches: 658 04.778 Concernsive: 33
& a	1768 AAGCAGCTGACCGAGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG 1827 	Ferceic Similarity Query Match: DB:	: 89.77# 76.65# 1
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g &	581 TrpTyrGlnLeuGluLysGluProlleValGlyAlaGluThrPheTyrValAspGlyAla 600 2008 GCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGAGGGCGGGGCGGCAGAAG 2067	Qy 304 CGCGAG Db 41 ArgGlu	CGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCAGCGAGCGCGCGGGCCCGAGCGC 357 ArgGluLeuGlnValTrpGlyArgAspAsnAsnSerProSerGluAlaGlyAlaAspArg 60
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RESULT GNVWH3 HIV-1 r N; Conta	4 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate HTLV-III ins: endonuclease (EC 3.1); retropepsin (EC 3.4.23.16); RNA-directed DNA poly ess: human immunodeficiency virus type 1. HIV-1	Db 181 FroGly Oy 772 CTGACC Db 201 LeuVal	ProGlymeraspGlyProLysValLysGlnTrpProLeuInrGluGluLyslleLysAlla 200 CTGACCGCCATCTGCGGGGGAGTGGAGAGGAGGGCAAGATCACCAAGATCGGCCCCGAG 831
A, Note C, Date C, Acces R, Ratne	A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03965 R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora	Oy 832 AACCCC	AACCCTACAACACCCCGTGTTCGCCATCAAGAAGAACAACACCACCAAGTGGCGCAAG 891
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Db 641 AsnGlnLysThrGluLeuGlnAlaile Qy 2152 AACATCGTGACCGACACCCAGTACGCCC				RESULT 5 T09440 pol polyprotein - human immunodeficiency C.Species: human immunodeficiency virus t	C; Accession: T09440 R; Pang, S.; Vinters, H.V.; Akashi, T.; O's submitted to the EMBL Data Library, July	A; Mcression: 109440 A; Accession: 109440 A; Status: preliminary; translated from GB A; Molecule type: DNA A; Molecule type: DNA	A; Cross references: UNIPROT: Q75755; EMBL: C; Genetics: A; Genetics:	Alignment Scores: 1.99e-153 Le	SCOLE: STATE OF THE COLE STATE OF THE COLE BEST LOCAL SIMILARITY: 90.15% Mis Othery Match: 76.17% Inc. 176.17% The Cole of the	09-610-313B-30 (1-2469) x T09440 (1-	Oy 220 TTCTTCCGCGAGGACCTGGCCTTCCCCC	Oy 280 AACCGCGCGACGCCCACCACCGCGCGCCGCCGCCGCCGCC	Qy 334 CGCAGCGAGGCCGGCGCCGAGGCCCAGG	OY 388 CTGTGGCAGCGCCCCTGGTGACATCJ 	Oy 448 GACACCGGCGCGACGACCACCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	Oy 5.08 AAGATGATGGGGGGATCGGCGGCTTCJ 	Oy 568 GAGATCTGCGGCAAGAAGCCATCGGC
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                                                                                                                               RESULT 7
GNVWA2
HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate ARV-2)
N; Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
C; Species: human immunodeficiency virus type 1, HIV-1
A;NOte: host Homo sapiens (man)
C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C; Date: 17-May-1985 #sequence and expression of an AIDS-associated retrovirus (ARV-2).
A; Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A; Reference number: A04003; MUID:85090453; PMID:257827
A; Residues: 1-1003 <SAN>
A; Residues: 1-1003 <SAN>
A; Cross-references: UNIPROT:P03369; GB:K02007; NID:G328658; PIDN:AABS9876.1; PID:G328662
C; Comment: Specific enzymatic cleavages may yield mature proteins including protease, re C; Genetics:
A; Gene: pol
C; Superfamily: pol polyprotein
C; Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nuclec
F; 57-147/Product: retropepsin #status predicted <RTP>
F; 81/Active site: ABP (shared with dimeric partner) #status predicted
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Score: 3477.00 Matches: 651	319GGCGGCGACAACCCCGCAGGGCCGGCGGCCGAGGGCCAGGGCACCCTG	490 CCCGGCAAGTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGA	14 ProfintPiroValAbnilellediyArgAbniceLeutningInlieclyCyStintrechash 14 ProfintPiroValAbnilellediyArgAbniceLeutningInlieclyCyStintrechash 164 PheProileSerProileGluThrValProValLysLeuLySProGlyMetAspGlyPro 164 PheProileSerProileGluThrValProValLysLeuLySProGlyMetAspGlyPro 1730 AAGGTGAAGCTGAGCCCCTGACCGCCTGAGCCCCCTGACGCCCTGACGCCCTGAGGAGGAACATCAGGCCCTGACGCCCTGAGGGGGAGGAACATCAGGCCCTGACGCCTGAGGGGGGGG
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Qy 1708 TTCAAGAACCTGAAGACGCCAAGATGCGCACCGCCCACCCA	1948 TGGTGGAGAGAGAGCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCCGCCGT	DD 0.21 ValValSeTileAlaAspinFinrAsHolinLySinrColuceUcinAlaileHisbeutal 0.40	681 IleLysLysGluLysValTyrLeuAlaTrpValProAlafisLysGlyIleGlyGlyAsn 700 2308 GAGCAGATCGACAGCCAGGCAAGGCCAAGGTCCTGTCTCGACGCATC 2367 701 GluGlnValAspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAsnGlyIle 720 2368 GAT 2370 721 Asp 721 SULT 8 SULT 8 Contains: endonuclease (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LV) Contains: endonuclease (EC 3.4.23.16); RAN-directed DNA pospecies human immunodeficiency virus type 1, HIV-1 Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 Accession: A03087 Musesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. Litle: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retro Reference number: A93355; MUID:85111157; PMID:2982104 Accession: A03057 Molecule type: DNA Residues: 1-1012 AMID: Residues: 1-1012

Db 684 GlnIleIleGluGlnLeuIleLysLy Qy 2290 AAGGGCATCGGCGCAACGAGCAACA Db 704 LysGlyIleGlyGlyAsnGluGlnVa Qy 2350 CTGTTCCTGGACGATCGAT 2370 Db 724 LeuPheLeuAspGlyIleAsp 730 RESULT 9 GNLJSI HIV-1 retropepsin (EC 3.4.23.16) - simia N;Contains: endonuclease (EC 3.1); r C;Species: simian immunodeficiency virus A;Nocte: host Pan troglodytes (chimpanzee C;Date: 30-Sep-1991 #sequence_revision 3.50, thost pandon 2.50, thost pandon	Nature: 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Alignment Scores: 2.73e-142 L Pred. No.: 3.249.00 M Score: Becrent Similarity: 89.46% C Best Local Similarity: 80.95% M Query Match: 1.089% I US-09-610-313B-30 (1-2469) x GNLJSI (1-1) QY 159 CTGCTGGAAGTGCGGCAAGGGGCC	Db 7 ieuLeùalavairrpalaargdiyTh Qy 219 CTTCTTCCGCGAGGCCTGGCCTTCC	Oy 333 CCGCAGCGGGCGGCGCGAGCGCCGAGCGCCCGAGCGCCCCCC
	1450 CTGGTGGCCAACTGGGCCAGATCTACCCCGGCATCAAGGTGCGCCACTG 1509 424 LeuValGlyLysLeuAenTrpAlaSerGlnIleTyrProGlyIleLysValArgGlnLeu 443 1510 TGCAAGCTGCTGCGGGGCCCAGACCCTGACCGACTGTGCCCTGACCGAGGGGGC 1569 1510 TGCAAGCTGCTGCGGGGCCCAGAGCCCTGACCGACACTCGTGCCCTGACCGAGGGGGC 1569 444 CysLysLeuLeuArgGlyThrLysAlaLeuThrGluValIleFroLeuThrGluGluAla 463 1570 GAGCTGGAGCTGCGGAGATCCTGGCGGGGCCGTGCCGGGGTGTACTAC 1629 1646 GluLeuGluLeuAlaGluAsnArgGluIleLeuLysGluProValHisGlyValTyrTyr 483 1630 GACCCCAGCAGGACCTGGTGGCGGGAGTCCAGAGGCCCACGGCGTGCACTAC 1689 1631 GACCCCAGAGGACCTGGTGGCGGGAGTCCAGAGGCCCACGGGGCCACTAC 1689 1640 HARPFOSETLYSASPLEUIILEAlaGluIleGlnLysGlnGlyGlnTrpThrTyr 503		1870 ACCTGGTGGACCGACTACTGGCAGCCCCCGAGTGGGAGTTCGTGAACACC 1929	604 Phelyrvalabelililililililissississississississississ
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us SIVcpz
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377; PMID:2188136
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EMBL: Z11530; NID: 960192; PIDN: CAA77622.1; PID: 960194
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Spanson immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: no. 33380
C;Accession: 33380
R;Carlini, F.
Submitted to the EMBL Data Library, November 1991
A;Reference number: 33379
A;Accession: 33380
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-912 <CAR>
A;Residues: 1-912 <CAR>
A;Cross-references: UNIPROT:Q78241; EMBL:Z11530; NID:g60192; PIDN:CAA77622.1; PIC;Superfamily: pol polyprotein
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                  CCGCAACATGCTGACCCAGCTGGACCTCGAACTTCCCCATCAGCCCCATCAGAGAC
                                                                                                                        CGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCCAAGGTGAAGCAGTGGCCCCTGAC
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    CTGCGGCAAGAAGGCCATCGGCACCGTGATCGGCCCCCACCCCGTGAACATCATCGG
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481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCGTTCATCAAG 540		ValLysGlnTyrAspGlnIleAlaIleGluIleCysGlyHisLysAlaIleGlyThrVal	601 CTMATCGGGCCCCGGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGC 660 :::	ACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG	ThrLeuAsnPheProlleSerProlleGluThrValProValLysLeuLysProGlyMet	721 GACGGCCCCAAGGTGAACCAGTGGCCCTGACCCAGGAGAAGATCAAGGCCCTGACCGCC 780 	ATCTGCGAGGAGGAGGAGGAGGGCAAGATCACCAAGATCGCCCCCGAGAACCCCTAC	 101 IleCysThrGluMetGluLysGluGlyLysIleSerLysIleGlyProGluAsnProTyr 120	841 AACACCCCGTGTTCGCCATCAAGAAGACGACAGCACCAAGTGGGCGCAAGCTGGTGGAC 900	121 AsnThrProValPheAlaileLysLysLysAspGlyThrLysTrpArgLysLeuValAsp 140	901 TTCCGCGAGCTGAACAAGCGCACCCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC 960	FIRST SOLUTIONS AND SOLUTIONS OF THE STREET SOLUTIONS OF THE SOLUTIONS OF		AGGGTGCCCTGGACGAGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAAC 1		1081 AACGAGACCCCCGGCATCCGCTACCAGTACATGCTGCCCCAGGCTGGAAGGCAGC 1140	201 AsnGluThrProGlylleArgTyrGlnTyrAsnValLeuProGlnGlyTrpLysGlySer 220	1141 CCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCC 1200	221 ProAlailePheGlnAlaSerMetThrLysileLeuGluProPheArgLysGlnAsnPro 240			CAGCACCGCCCAAGATCGAGGAGCTGCGCACCTGCTGCGCTGCGCTTCACCACC	251 GINHIBARGINELYBELEGINGENDENARGARGHIBLENDENARGIIDGIYFNEINFIN 280 1321 CCCGACAAGAACACCAGAAGGAGCCCCCTTTCTTGAGAATGAGTTACGAGTTGCAACTC 1380		GACAAGTGGACCGTGCACCATCGAGCTGCCCGAGGAGGAGGAGGTGGACCGTGAACGAC		1441 ATCCAGAAGCTGGTGGAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG 1500	321 IleGinLysLeuValGlyLysLeuAsnTrpAlaSerGinIleTyrAlaGlyIleLysVal 340	1501 CGCCAGCTGTGCAAGCTGCTGCGCGGCCCAAGGCCCTGACCGACATCGTGCCCTGACC 1560	341 ArgGlnLeuCysArgLeuLeuArgGlyAlaLysAlaLeuThrGluValIleProLeuThr 360	1561 GAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGC 1620
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Aain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
C. variability of the AIDS virus: Nucleotide sequence analysis of two isoluber: 214389; MUID:86245056; PMID:2424612

lated from GB/EMBL/DDBJ : mrna

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ces: EMBL:K03456; NID:g60228; PIDN:CAA28012.1; PID:g60230
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Oy 1471 GCCAGCCAGATCTACCCCGGCATCAAGGT	361	381	Oy 1711 AGARACCTGAAGACGGCAAGTACGCAA 	1771	1831	Oy 1891 CAGGCCACCTGGATCCCGAGTGGGAGTT	Oy 1951 TACCAGCTGGAGAGGCCCATCATCGC	Oy 2011 AACCGCGACACCAAGATCGGCAAGGCCGG	Oy 2071 GTGAGCCTGACCGAGGACCACCAGAN	Qy 2131 CAGGACAGCGAGGTGAACATCG7 	Qy 2191 CAGGCCCAGCCGACAAGAGGGAGGGGGGGGGGGGGGGG	2251	Oy 2311 CAGATCGACAGCTGAGCAAGCAAGCACACACACACACACA	RESULT 12 B47175 reverse transcriptase, AZT-sensitive variar C;Species: human immunodeficiency virus tyr	C;Date: 21-Jan-1994 #Bequence_revision 18-7 CAccession: B47175 R;Aonti, H.; Singh, M.K.; Ching, W.T.; Ho, Proc. Natl. Acad. Sci. U.S.A. 90, 25-29, 19	A,Title: Quantitation of zidovudine-resists A,Reference number: A47175, MUID:93126353, A,Accession: B47175 A,Status: preliminary, nucleic acid sequenc
. No.: 6.48e-137 3132.00 312.00 312.00 500 Similarity: 97.74% 68.34% 7 Match: 68.34%	US-09-610-313B-30 (1-2469) x T01668 (1-902) Qy 511 ATGATCGGCGCGATCGGCGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAG 570	Oy 571 ATCTGCGGCAAGAGCCATCGGCACCGTGGTGATCGGCCCCCCCGTGAACATCATC 630	Qy 631 GGCCGCAACATGCTGACCTGGGCTGCACCTGAACTTCCCCATCAGCCCCATCAGG 690	691 ACCGGGCCGGGAAGCTGAAGCCCGGCAAGGTGAAGGAGGGGGCCCCTG	Oy 751 ACCGAGGAGAAGATCAAGGCCCTGACGCGATCTGCGAGAGATGGAGAAGGGGGGAAG 810	Qy 811 ATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCGTGTTCGCCATCAAGAAGAAG 870	871 GACAGCACCAAGTGGGGACTGGACTTCGGGAGCTGAACAAGCGCACCCAGGAC 93	121 ASSETTITURY SITEMPRINA THE TRANSPORTED CONTROLL OF THE STATEMPRINA THE TRANSPORTED STATEMPRINA THE TRANSPORTED STATEMPRINA THE STATEMPRINA THE STATEMPRINA THE STATEMPRINA THE STATEMPRINA THE STATEMPRINA THE STATEMPRINA STATEMPRINA THE STATEMPRINA STATEMP	991 ACCGTGCTGGACGTGGCGACGCTACTTCAGCGTGCCCCTGGACGAGACTTCCGCAAG 1	1051 TACACCCCTTCACCATCCCCACCATCAACAACAACAACACCAC	1111 AACGIGCTCCAGGGCTGGAAGGCCAGCCCAGCATTTCCAGAGCAGCATGCAAG 1	1171 AFCCTGGGGCCGGCAGCCCGGAGTCCGGATCTACGAGTAGTGGGCGC 12 221 Ill		1291 AAGCACCTGCTGCGCGGCGCTTCACCCCCGCACAAAAAAGACCCCCCCC	51	Oy 1411 CCCGAGAAGGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGG 1470 :::

GAGCTGGTGAACCAGATCCAGCGAGCTGATC 2250 ATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370 GGCGCCGAGACCTTCTACGTGCACGGCGCCGCC 2010 GTGACCGACAGCCAGTACGCCCTGGGCATCATC 2190 GTGCCCGCCACAAGGGCATCGGCGGCAACGAG 2310 GGCCTGTACTACGACCCCAGCAAGGACCTGGTG 1650 CAGTGGACCTACCAGATCTACCAGGAGCCCTTC 1710 Tregrandacecececeregrandering 1950 GGCTACGTGACCGACGGGGCCGGCAGAAGATC 2070 AAGACCGAGCTGCAGGCCATCCAGCTGGCCCTG 2130 GIGCGCCAGCIGIGCAAGCIGCTGCGCGCGCCC 1530 ACCGAGGAGGCCGAGCTGGACGAGAAC 1590 AAGATGCGCACCCCCACACCACGACGTGAAG 1770 arglleLysSerAlaHisThrAsnAspValLys 420 540

ant - human immunodeficiency virus type 1, HIV-1 -Nov-1994 #text_change 09-Jul-2004

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), D.D. 11993 start human immunodeficiency virus type 1 in the s; PMID:7678340

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C. Species: human immunodeficiency virus type 1, HIV-1
C. Species: n-69-193 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C. Accession: A47175
R. Mohri, H.; Singh, M.K.; Ching, W.T.; Ho, D.D.
R. Mohri, H.; Singh, M.K.; Ching, W.T.; Ho, D.D.
R. Mohri, H.; Singh, M.K.; Ching, W.T.; Ho, D.D.
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R. Mcference number: A47175; MUID: 93126353; PMID: 7678340
A. Reference number: A47175; MUID: 93126353; PMID: 7678340
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C. Superfamily: pol polyprotein
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A;Residues: 1-559 <MOH>
A;Cross-references: UNIPROT:09PXX1
A;Note: sequence extracted from NCBI
C;Superfamily: pol polyprotein
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		Qy 1933 CCCCTGGTGAGCTGTGGTAGCAGCTGGAGAGCCCTCTCTCT	Db 461 iysGlyArgGlnLysValValSerLeuThrAspThrThTAsnGlnLysThrGluLeuGln 480	Qy 2233 ATCATGAGCAGCTGATCAAGAGAGAAGGTGTACCTGAGCTGCCGCCCACAAG 2292 Db 521 IleIleGluGluLeulleLysGluLysValTyrLeuAlaTrpValProAlaHisLys 540 Qy 2293 GGCATCGGCGAACGAGTACGACAAGCTGAGCATCCGCAAGGTG 2349 Db 541 GlylleGlyGlyAsnGluGlnValAspLysLeuValSerAlaGlyIleArgLysVal 559	\$46347 pol polyprotein - simian immunodeficiency virus SIVagm (isolate SAB-1) C;Species: simian immunodeficiency virus SIVagm C;Species: simian immunodeficiency virus SIVagm A;Variety: isolate SAB-1 C;Date: 25-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999 C;Accession: 546347 R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.; P EMBO J. 13, 2935-2947, 1994	A; Reference number: \$46335; WUID:94298785; PMID:8026477 A; Accession: \$46347 A; Status: nucleic acid sequence not shown; translation not shown A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-1039 A; Residues: 1
Pred. No.: 3.66e-121 Length: 559 Score: 2789.00 Matches: 514 Percent Similarity: 96.60% Conservative: 26 Best Local Similarity: 91.95% Mismatches: 19 Query Match: 2 0 Gaps: 0 DB: 2 CA469) x A47175 (1-559) Qy 673 CCCATCAGACCCCATCAGACCCCTGAAGCTGAAGCTGAAGCTCCAAG 732 Qy 673 CCCATCAGACCCCATCAGACCCCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTCAAG 732 Db 1 ProllederProlledluThraalProvalbysProGlyMetAspOlyProLyg 20	733 GTGAAGCACTGGCCCCTGACCGAGGAGAAGAATCAAGGCCTGACCGCCATCTGCGAGGAGAGAGA	853 TTGGCCATCAAGAAGAAGAAGCACCCAAGTGGCGAAGCTGGTGGACTTCCGCGAGGCTG [101 LysLysLysLyslerCollection Collection Col	Db	1273 201 1333 221	41 ValGinProliteValLeuProGluLysAspSerTrpThrValAsnAspileGlnLysLeu 260 42 ValGinProliteValLeuProGluLysAspSerTrpThrValAsnAspileGlnLysLeu 260 43 GTGGGCAAGCTGAAGGCCAGCAAGTCTACCCGGCATCAAGGTGCGCCAGCTGTGC 151. 44 ValGinProliteValLeuProGluLysAspSerTrpThrValAspileGlnLysLeu 260 45 GTGGTGCTGCGCGCGCAGCCCTGACCGACACTCGTGCCCTGACGAGAGGCCGAG 157. 46 CTGGTGCTGCGCGCGCCCTAACGCCCTGACCGAGAGGCCGAG 157. 47 AAGCTGCCGGCGCGCCCTAACGACCCTGACCGAGAGGCCGAG 157. 48 LysLeuLeuArgGlyThrLysAlaLeuThrGluVallieGlnLeuThrGluAlaGlu 300 49 TGGAGCTGGCCGAGAACCGCGAGATCCTGGCCGTGCCCGTGACGAGAGCCCGTGACGAGACCGCGTGACACACGACGAGACCCGGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGGCGAGAACCGCGAGAACCGGCGAGAACCGCGAGAACCGCGCGAGAACCGCGAGAACCGCGAGAACCGGCGAGAACCGGCGAGAACCGCGAGAACCGCGAGAACCGCGAGAACCGCAGAACCGCAGAACCGCAGAACCGCAGAACCGCAGAACCGCAGAACCGCAGAACACACAACA

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537 CAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCAC 596 158 eAsnThrLysGluTyrLysAsnValGluTleGluValLeuGlyLysArgValargalaTh 178 1597 CGTGCTGATCGGCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCTGGG 656 178 filemetThrGlyAspThrProileAsnIlePhedlyArgAsnIleLeuThrAlaLeuGl 198 657 CTGCACCCTGAACTCCCCATCGACCCCTGCACGTGCCGGG 716 158 yMetSerLeuAsnLeuProValalaLysIleGluProileLysIleMetLeuLysProGl 218		298 OHisProhlaGiyjeunlaiysiyshrghrgliethrvaileeukspvalGlyhsphalafy 318 1017 CTTCAGCGCCCCTGGACGACTTCCGCAGTTCACCCTTCACCATCCCCACAT 1076 318 rPheser: Tiel
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CGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAGAGACCAAGATCGGCAAGGC 2036
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-FRANDITAL20 -WARN TIMEOUT=1.0 -YGAPOF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Adp84803 HIV-1 hyb
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Aab69289 HIV-1 non
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Aab69287 HIV-1 non
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11351.628 Million cell updates/sec
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Aab86169 1
Aab69282 1
Aaw72993 1
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                           protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                                                       2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
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Jatabase :

3304.5 3782.5 3741.5 3658 3644 3644 3608 3608 3555.5

10 8 4 9 7 8 6 11

Score

No.

Result

Transcrip HIV-1 non

HIV pol AIDS

Pol prote

Human lym HIV-1 pol

WPI; 2004-191004/18 N-PSDB; ADS19485

Delivering exogenous (e.g. CFTR) genes to epithelial cells in the respiratory tract using a penetration agent and a lentiviral packaging system, useful for treating e.g. cystic fibrosis.

Disclosure; Fig 16; 45pp; English

g ò 8 a ð 셤 ò 셤 δ 엄 ò 셤 8 q ò 셤 ò g 8 g ò 셤 à 셤 ò 음 ò 셤 ò

The present invention relates to a method of delivering one or more exogenous genes for expression in an epithelial cell in the respiratory expension in an epithelial cell in the respiratory espensus designed of a mammal to give persistent expression of the gene in the epithelial cell, using a lentiviral packaging (expression vector) system. Also disclosed are (i) a recombinant lentiviral packaging system. Comprising a first nucleic acid molecule including a gag gene sequence conding a Gag protein, and a second mulcic acid molecule including a gagool gene sequence care for the charce of a frame shift which switches expression of the Gagool protein to the Gag protein in wild type lentivirus and the packaging system additionally comprises a lentiviral vector nucleic acid molecule which does not encode either the gag gene or the gagol gene is expression of the Gag protein in the wild type lentivirus. The exogenous gene is expressed in sufficient numbers of cells and amounts to provide an ameliorating effect for a respiratory condition. The exogenous gene is expressed in sufficient unmbers of cells and amounts to provide an ameliorating effect for a respiratory condition. The exogenous gene is orbitated cells, non-cillated cells, secretory cells and basal cells. The exogenous gene is orbitated cells, non-cillated cells, secretory cells and basal cells. The exogenous gene may be enably differentiated and is capalle or differentiating which descendinant lentivirus carrying an exogenous gene to the respira

Sequence 1435 AA;

Length: Matches: Conservative: Mismatches: Indels: Gaps: 8.15e-215 3804.50 94.82% 89.25% 83.01% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

JS-09-610-313B-30 (1-2469) x ADS19486 (1-1435)

- TTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCC 129 402 69 13 ATGGCCGAGGCCATGAGCCAGGCCACC---AGCGCCAACATCCTGATGCAGCGCAAC 70 383 ઠે 유 g ઠે
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190 423 250	ATGAAGGACTGCACCGAG
+ + 9	crecagergecgcgcgcgacaaccccggagagagagagcgggggggg
364	CTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAG 4.
418	GTGGGCGGCCAGATCAAGGGCCCTGCTGGACACCGGCCCGACGACACGTGCTGGAG 47:: :::
478	GAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATC 53
538	AAGGTGGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACC 59
598	GTGCTGATCGGCCCCACCCCGTGAACATCATCGGCCGCA :::
658 583	TGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGC 71.
718	AIGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACC 77
778	GCC
838	TACAACACCCCGTGTTCGCCATCAAGAAGAACGACACCAAGTGGCGCAAGCTGGTG 89
898	GACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCC 9
958	CACCCCCCCCCCCCAAAAAAAAAAAAACCTCATAACCGTCCTCGAACGTGGCCCAACCTAC 10
1018	TTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATC 10
1078	AACAACGAGGACCCCGGGGATCCGGTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGC 1
1138	AGCCCCAGCATCTTCCAGAGCAGCATCACCAAGATCCTGGAGCCCTTCCGCGCCCCCCCC
1198	CCCGAGATCGTGATCTACCAGTACATGGACCTGTACGTGGGCAGCGACCTGGAGATC 12
1258	GGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGC

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US-09-610-313B-30 (1-2469) x ADP84803 (1-3183)
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                                ACCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCAC 1377
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                                                                                                                                                                                                                                                                                                                                      1738 AAGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATC 1797
                                                                                                                              923 GlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeuLysThrGlyLysTyrAla 942
                                                                                                                                                                                                                                                                                                                                                           962
                                                                                      ThrProAspLysLysHisGlnLysGluProProPheLeuTrpMetGlyTyrGluLeuHis
                                                                         CCCGACAAGTGGACCGTGCCCCATCGAGCTGCCCGAGAAGGAGGAGCTGGACCGTGAAC
                                                                                                                   GACATCCAGAAGCTGGCCAAGCTGAACTGGGCCAGCCAGATCTACCCCCGGCATCAAG
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The invention relates to a novel method for eliciting or inducing in a mammal an immune response directed to a virus, preferably Human immunodeficiency virus (HIV). The method comprises sequentially administering to the mammal one or more sequential doses of a recombinant plasmid vector or recombinant viral vector or its derivative, into which the nucleic acid molecules encoding all, part or a modified form of two or more antigens of the virus are incorporated, and one or more optimized or more antigens of the virus are incorporated, and one or more optimized or more antigens of the virus are incorporated, and one or more optimized or more antigens have been rendered substantially nonpathogenic. The invention further comprises: a method for treating or preventing viral pathogen; a method of eliciting or inducing an animal, an immune response directed to HIVs a vaccine capable of inducing an immune response directed to HIVs comprising the recombinant plasmid to vector or recombinant viral vector or its functional derivative; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid, plasmid vector or recombinant viral vector constructs. The method is useful in eliciting or inducing in a mammal an immune response against HIV-I subtype AE, B or C. This sequence represents the protein of the HIV-1 hybrid isolate pNL4-3 DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eliciting or inducing in a mammal an immune response against HIV-I subtype AE, B or C by administering sequential doses of a recombinant plasmid and viral vectors containing the nucleic acid molecules encoding the HIV antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid construct or its functional derivative comprising the plasmid vector or recombinant viral vector; a plasmid vector; a recombinant viral vector; a pharmaceutical composition comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramshaw IA;
                                                                                                                                                                                                                             response; HIV; antigen; non-pathogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramsay A, Thomson S,
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
1143 IleArgLysValLeuPheLeuAspGlyIleAsp 1153
                                                                                                                                                                                       HIV-1 hybrid isolate pNL4-3 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boyle DB,
                                                                         ADP84803 standard; protein; 3183
                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-2002; 2002AU-00953556.
17-SEP-2003; 2003AU-00905067.
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                                                                                                                                                                                                                             eliciting; inducing; immune vaccination; vaccine; HIV-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kent SJ, Purcell DF,
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                08-JUL-2004
                                                                                                               ADP84803;
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DB:
                                                       ADP84803
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us-09-610-313b-30.n2p.rag

Percent Similarity: 92.24* Conservative: 28 Best Local Similarity: 88.74* Mismatches: 44 Query Match: 81.64* Indels: 19 DB: 8 Gaps: 3 US-09-610-313B-30 (1-2469) x ADN36406 (1-1457)	Qy /13 ATGGCCGAGGCCATGAGCCACCAGGCCACACATCCTGATGCAGCGCAGCAACTTC 72 :::	Oy 73 AAGGGCCCCAAGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGCCACATCGCCCGC 132	Qy 133 AACTGCCGCGCCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAAGGGCCACCACATG 192 Db 422 ABnCysArgAlaProArgLysLysGlycYsTrpLysCysGlyLygYugGluGlyHisGlnMet 441	Qy 193 AAGGACTGCACCGAGGCCAACTTCTTCCGCGAGGACCTTCCCCCAGGGC 252	Qy 253 AAGGCCGGGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGGAGTG 312	OY 313 CAGGGGGGGGACAACCCCCGGAGGGGGGGGGGGGGGGG	Qy 373 TTC	Db 501 rSerLeuLygSerLeuPheGlySerAspProLeuSerGlnProGlnIleThrLeuTrpGl 521	GACACCGG	erileArgValGlyGlyGlnileLysGluAlaLeuLeu 53	F=	Db 539AspAspThrValLeuGluGluValAsnLeuProGlyLysTrpLysProLysMetIl 557	Qy 516 CGGCGGCATCGGCGGCTTCAACGTGCGCCAGTACGACCAGATCCTGATCGAGTCTG 575	Db 557 eGlyGlyIleGlyGlyPhelleLysValArgGlnTyrAspGlnIleProileGlulleCy 577		CGAGACCGT	597	Qy 696 GCCCGTGAAGCTGAAGCTCGGCATGGACGCCCCAAGGTGAAGAGTGGCCCCTGACCGA 755	Oy 756 GGAGAAGATCAAGGCCTGACCGCCATCTGCGAGGAGATGAAGAAGAAGAAGAAGATCAC 815	Db 637 uGluLysIleLysAlaLeuThrAlaIleCysAspGluMetGluLysGluGlyLysIleTh 657	Qy 816 CAAGATCGGCCCCGAGAACCCCTACAACACCCCCTGTTCGCCATCAAGAAGAAGAAGG 875 Db 657 rLys1leGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLysLysAspSe 677	Oy 876 CACCAAGTGGCGCAAGTGGTGGACTTCCGCGAGCTGAACAAGCGCACCACGACTTCTG 935	Db 677 rThrLysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTr 697	Qy 936 GGAGGTGCAGCTGCCCCACCCCGCCGGCCTGAAGAAGAAGAGGGGGCGT 995
	Qy 2074 AGCCTGACGAGACCACCAGAAGACCGAGCTGCAGCCATCCAGCTGGCCCTGCAG 2133 Db 1123 ProLeuThrAspThrThrAsnGlnLysThrGluLeuGlnAlaileHisLeuAlaLeuGln 1142	Qy 2134 GACAGCGGCAGCGAGGTGAACATCGTGACCGACCAGTACGCCCTGGGCATCATCCAG 2193 Db 1143 AspSerGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGln 1162	Qy 2194 GCCCAGCCGACAAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAG 2253 Db 1163 AlaGlnProAspLysSerGluSerGluSerGluLeuValSerGlnIleIleGluGlnLeuIleLys 1182	Qy 2254 AAGGAGAAGGTGTACCTGAGCTGGCCGCCCCACAAGGGCATCGGCGGCAACGAGCAG 2313	Qy 2314 ATCGACAAGCTGGTGAGCAATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370 :::	RESULT 3 ADN36406 ID ADN36406 standard; protein; 1457 AA.	XX AC ADN36406;	XX DT 15-JUL-2004 (first entry)	XX DB Human protein for anti-HIV vaccine. XX	W anti-HIV; vaccine; HIV; promoter; viral particle; immunization.	Homo sapiens.	MO2004035006-A2.	29-APR-2004.	PF 17-OCT-2003; 2003WO-US033112.	18-OCT-2002; 2002US-0419465P.	PA (AARO-) AARON DIAMOND AIDS RES CENT. KX THO DD, Chen Z:	WPI; 2004-348328/32. N-PSDB; ADN36405.			בופרדוספודפי ספק זה אס פסי דפסקה.	CC The invention relates to a nucleic acid vector comprising at least one CC HIV sequence operably linked to a promoter and encoding a protein that CC does not assemble into viral particles. The nucleic acid vector is useful CC in immunizing a subject against HIV infection. This sequence corresponds			Alignment Scores: 4.08e-211 Length: 1457 Pred. No.: 3741.50 Matches: 709

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1157 2315

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Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number of human immunodeficiency virus (HIV) type I non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                          CCAGCCCGACAAGAGCGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA
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                                                            CAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGC
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Mismatches:
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nucleotide sequence.
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Query Match: 79.82% Indels: 0 DB: 3 Gaps: 0 US-09-610-313B-30 (1-2469) x AAB69289 (1-1003)	220 TICTICGGGAGGACCTGGCCTTCCCCCAGGGCCAAGGCCCGCGAGTTCCCCAGCGAGCAG 279	c v—	21 AlaArgAlaAsnSerProThrSerArgGluLeuGlnValGlnGlyAspAsnProArgSer 40 340 GAGGCCGCCGGGCCCAGGGCCCAGAACTCCCCCAGATCACCCTGTGGCAGGC 399	CCCCTGGTGAGCATCAGGGCGCCAGATCAAGGAGGCCCTGCTGGACACCGGGGCCCTGCTGGTGAGCACCCGGGGCCCTGCTGGACACCGGGGCCCTGCTGGACACCGGGGCCCTGCTGGACACCGGGGCCCTGCTGGACACCGGGGCCCTGCTGGACACCGGGCCCCTGCTGGACACCTGCTGGACACCGGCGCCCTGCTGGACACCTGCTGAACACCTGCAACACCTGCAACACCTGCAACACCTGCAACACACAC	FIGURE WAISE LITER SATELY STREET SET THE STREET SET THE STREET SET THE STREET SET THE STREET SET SET THE STREET SET SET SET SET SET SET SET SET SET	GGCATCGGCGCCTTCATCAAGTGCGCCGCTACGATCTCAACGCGC S	AGAAGGCCATCGGCACCGTGTGTGGCCCCCCCGTGAACATCATCGGCCGCAAC 6	69	GTGAAGCTGAAGCCCGGCAGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAG 7	AGGAGATGGAGAGGGCAAGATCACCAAG 8 	820 ATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGAACGCACC 879	93	GTGCAGCTGGGCTTCCCCCCCCCCCGCCGGAGAAGAAGAAGAAGAGCGTGCCGGGGGGGG	1000 GACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGACTTCCGCAAGTACACCGCC 1059 	TTCACCATCCCCAGCATCAACAACAGACCCCCGGCATCCGCTACCAGTACAACGTG 1		CCCTTCGGCGCCGCACCCGGGATCGTGATCTACCAGTACATGGACGACCTGTACGTG 1
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AAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGGAAGAGGCAAGATCACCAAG
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                                                                                                                                                                                                                                                                                                                                                                               The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B solutes. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies gainst non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                      env; vpu;
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useful for detecting
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Best Local Similarity:
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vif; vpr; tat
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Pred. No.:
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IleTyrAlaGlyIleLysValArgGlnLeuCysLysLeuLeuArgGlyAlaLysAlaLeu
               ACCGACATCGTGCCCCTGACCGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATC
                        ThrAsp11eValProLeuThrGluGluAlaGluLeuGluLeuAlaGluLeaBluE
                                              CTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATC
                                                    CAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTG
                                                                                      GlnLysGlnGlyHisAspGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeu
                                                                                                           AAGACCGGCAAGTACGCCAAGATGCGCACCCCCACCAACGACGTGAAGCAGCTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV-1; human immunodeficiency virus; non-subtype vif; vpr; tat; rev; nef; vaccine.
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                                                                                                  The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
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of non-subtype B human immunodeficiency and treating AIDS comprises a specific
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                                                                      Claim 41; Fig 15; 131pp; English
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97.23%
94.74%
79.51%
                                     nucleotide sequence.
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Best Local Similarity:
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        GGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACC
                                       AAGCTGTGGTACCAGCTGGAGAAGGAGCCCCATCATCGGCGCCGAGACCTTCTACGTGGAC
                                                                                                  601 GlyAlaAlaAsnArgGluThrLysIleGlyLysAlaGlyTyrValThrAspArgGlyArg
                                                                                                                                                       CAGAAGATCGTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAGGCCATCCAG
                                                                                                                                                                                     CTGGCCCTGCAGGACAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTG
                                                                                                                                                                                             641 LeuAlaLeuGlnAspSerGlySerGluValAsnIleValThrAspSerGlnTyrAlaLeu
                                                                                                                                                                                                                  2182 GGCATCATCCAGGCCCAGCCCGACAAGAGCGAGGCGAGCTGGTGAACCAGATCATCGAG
                                                                                                                                                                                                                          Regulatory gene; accessory gene; HIV; human immunodeficiency virus; vaccine; infection; gene therapy; reverse transcriptase; RT; enzyme.
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                                                                     ATGGACGACCTGTGGGCAGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAG
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                                        TGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGAGATGGAGAAG
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N-PSDB; AAD29258.

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New molecules comprising HIV-1 subtype isolate regulatory/accessory
PT genes, useful for manufacturing a vaccine for treating or preventing HIV

infection.

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Disclosure; Page 94-97; 97pp; English.

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The invention relates to molecules comprising HIV-1 subtype isolate
C regulatory/accessory genes (tat, nef and rev genes) and modifications and
C derivatives thereof. The invention also provides proteins encoded by such
C derivatives of the invention are useful for manufacturing vaccines
CC derivating or preventing human immunodeficiency virus (HIV) infections.

CC They are also useful in gene therapy. The present sequence is HIV-1

SUBJECT-2003 to standardise OS field)

Sequence 998 AA;
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Pred. No.:	2.54e-203	Length:	866
Score:	3608.00	Matches:	670
Percent Similarity:	97.63%	Conservative:	29
Best Local Similarity:	93.58%	Mismatches:	17
Query Match:	78.73\$	Indels:	0
DB:	9	Gaps:	0
US-09-610-313B-30 (1-2469) x AAE37601 (1-998)	(69) × AAE37601	(1-998)	

US-09-610	-313E	-09-610-313B-30 (1-2469) x AAE37601 (1-998)
ò	223	TTCCGCGAGGACCTGCCCTCCCCCAGGCCAGAGGCCCGCGAGTTCCCCAGCGAGCAGAAC 282
QQ Q	H	
È	283	CGCGCCAACAGCCCCACCAGCCGCGGAGCTGCGCGCGGCGACAACCCCCGCAGCGAG 342
Dp	21	ArgalaAsnSerProThrSerArgGluLeuGlnValArgArgAsnAsnProArgSerGlu 40
È	343	GCCGGCCCGAGCGCCAGGCACCCTGAACTTCCCCCAGATCACCCTGTGGCGCAGCGCCCC 402
Q	41	ThrGlyAlaGluArgLysGlyThrLeuAsnPheProGlnIleThrLeuTrpGlnArgFro 60
È	403	CTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGAC 462
qq	61	LeuValSerIleLysIleGlyGlyGlnThrArgGluAlaLeuLeuAspThrGlyAlaAsp 80
È	463	GACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGC 522
qq	81	ASPThrValLeuGluAspIleAsnLeuProGlyLysTrpLysProLysMetIleGlyGly 100
à	523	ATCGGCGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAG 582
qq	101	IleGlyGlyPheIleLysValArgGlnTyrAspGlnIleLeuIleGluIleCysGlyLys 120
ò	583	AAGGCCATCGGCACCGTGATCGGCCCCACCCCCGTGAACATCGGCCGCAACATG 642
qq	121	LysAlalleGlyThrValLeuValGlyProThrProValAsnIleIleGlyArgAsnMet 140
È	643	CTGACCCAGCTGGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTG 702
qq	141	LeuThrGlnLeuGlyCysThrLeuAsnPheProlleSerProlleGluThrValProVal 160
È	703	AAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAAAG 762
Ωp	161	LysLeuLysProGlyMetAspGlyProLysValLysGlnTrpProLeuThrGluCluLys 180
ò	763	ATCAAGGCCCTGACCGCATCTGCGAGGAGGAGGAAGGAGGGCAAGATCACCAAGATC 822
Ωp	181	
ò	823	GGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAG 882
qq	201	GlyProGluAsnProTyrAsnThrPro11ePheAla11eLysLysLysAspSerThrLys 220

<u>ک</u> ۾	883	TGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAGCGCACCCAGGACTTCTGGGAGGTG 942
ò	4	TOTAL THE
qq	241	
<u>ک</u> ۾	1003	GTGGGCGACGCCTACTTCAGCGTGCCCTGGACGAGACTTCCGCAAGTACACCGCCTTC 1062
: &	9	CCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCC 11
අු	281	ThrileProSerileAsnAsnGluThrProGlyIleArgTyrGlnTyrAsnValbeuPro 300
È	0	11
q	301	/TrpLysGlySerProAlaIlePheGlnGlySerMetThrLysIleLeuGluPro 320
ራ 4	1183	TTCCGCGCCCGCAACCCCGAGATCGTGATCTACCAGTACATGGACCTGTAGGTGGGC 1242
'n	1243	GACCTGGAGATCGGCCAGCACGCGCCAAGATCGAGGAGTTGCGCAAGCACTTGCT
ΩÞ	341	
δ	1303	CGCTGGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTGTGGATG 1362
Db	361	:
à	63	
qq	381	oAspLysTrpThrValGlnProlleGlnLeuProGluLysAsp 400
à	1423	
QQ	401	erTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIl
ò	1483	TACCCCGGCATCAAGGTGCGCCAGCTGCAAGCTGCTGCGCGCGC
qa	421	ProglylleLysValArgGlnLeuCysLysLeuLeuArgGlyThrLysAlaLeuTh
ò	1543	SAGAACCGCGAGATCCTG 16
Ωp	441	sVal ProLeuThrGluGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLe
λ	1603	CGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAG 16
Db	461	GluproValHisGlyValTyrTyrAspProSerLysAspLeulleAlaGlull
ò	1663	AAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAG 1722
Dþ	481	31nGlyAspAspGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeuLy
ò	1723	ACCGCAAGTACGCCAAGATGCGCACCCCCCACACCAACGACGAAGCAGCTGAACGAG 1782
Ор	501	LeuThrGl
δ	1783	CAGAAGATCG
qa	521	laValGlnLyslleSerLeuGluSerIleValIleTrpGlyLysThrProLysPheAr
, Vo	1843	ATCCAGAAGG
Op.	541)rolleGlnLygGluThrTrpGluIleTrpTrpThrAgpTyrTrpGlnAlaTh
ķ	1903	ATCCCGAGTGGGAGTTCGTGAACACCCCCCCCTGGTGAACTGTGGTACAGCTGGAG 1962
qa	561	- a>

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induction of specific humoral and cellular immune responses. (I) and polypeptides (II) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus-1 (HIV-1) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype (CB' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in the method of the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGCCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTGCTGGAGGAGAT 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rLeuAsnPheProlleSerProlleGluThrValProValLysLeuLysProGlyMetAs
                                                                                                                                                                                                                                                                                                                                                                                                  |||||||||:::||||||
416 GlyArgGlyAsnGluProAsnLysGln---CysHisThrAspAlaGluLysGlnPhe***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   475 ArgLeuTyr***GluThrGlyGln-PhePheArgGluAsnLeuAlaLeuProGlnGlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCCGAGGCCATGAGCCAGGCCACCAGCCCAACATCCTGATGCAGCGCAGCAACTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          75 GGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           argieu***LysAsnCys***MetPheGlnLeuTrpGlnGlyArgAlaHisSerGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 GGACTGCACCGAGCCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCCAGGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCCACCAGCGCGCGAGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       494 gAlaArgGluPheSerSerGluGlnThrArgAlaAsnSerProThrArgGlyGluLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTG-----CGCGGCGACAACCCCCGCAGCGAGGCCGCGAGCGCCAGGGCACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 G-----AACTICCCCCAGAICACCCTGTGGCAGCGCCCCCTGTGGTGAGCTCAAGGTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 GAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGCGCATCGGCGCGTTCATCAAGGT
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Conservative:
Mismatches:
Indels:
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92.15%
86.84%
78.57%
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Best Local Similarity:
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                                                                                                                                                                                                                999
                                                                                                                                                                                                                                                                        680
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                                                                                                                                                LysGluProlleAlaGlyAlaGluThrPheTyrValAspGlyAlaAlaAsnArgGluThr
                                                                         AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACC
                                                                                      AGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCCAGCCC
                                                                                                                                                                                                                                                            GTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAG
                                                                                                                              GAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosis; human; humoral immune response; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                                                                                          CTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response; vaccine; treatment; gene therapy
                                                                                                                                                                                                                                                                                                                                                                         codon"
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GENEART GMBH GES ANGEWANDTE BIOTECHNOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .3025
/label= Xaa
/note= "Xaa represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB86169 standard; protein; 3025 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subtype C protein fragment #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 8A-O; 48pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Graf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH20870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE10056747-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1999;
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21-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infection;
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(GENE-)
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194 474 254 494 314 514 368 534 422 554

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The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tar, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                          Claim 41; Fig 15; 131pp; English.
                                                                                                                                                                                                                                                                                                                                         Sequence 1000 AA;
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937 GAGGTGCAGCTGGGCATCCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAAGAGCGTGACCGTG 996

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q	4	
k a	997	CTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACC 1056
දු යු	1057 281	GCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTG 1116
λ _o q	301	CTGCCCCAGGGCTGGAAGGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTG 1176
ž q	321	GAGCCCTTCCGCGCCCCCGCACCCCGAGATCGTGATCTACCAGTACATGGACCTGTAC 1236
g S	1237 341	GTGGGCAGGGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCAC 1296
oy Q	1297 361	CIGCIGCGCTGGGGCTTCACCACCCCGGCAAGAACACCACAGAAGGACCCCCCTTCCTG 1356
A q	1357 381	TGGATGGGCTACGACCCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAG 1416
DP GS	1417	AAGGAGACTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGC 1476
Qy Db	1477	CAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGC
ζζ Op	1537	CTGACCGACATGGTGCCCCTGACCGAGGCGGAGGTGGAGGTGGCCGAGAACCGCGAG 1596
P &	1597	ATCCTGCGGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAG 1656
<u>ያ</u>	1657	ATCCAGAAGCAGGCCACCACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAAC 1716
p &	1717 501	GCAAGTA SlyLysTy
b ç	1777 521	ACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAG 1836
b Q	1837	TTCCGCCTGCCCATCCAGAAGGAGCCTGGAGACCTGGTGGACCGACTACTGGCAGGCC 1896
QY Dp	1897 561	ACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCTGGTGAAGCTGTGGTACCAG 1956
oy Db	1957 581	CTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGC 2016
<u>۸</u>	2017	GAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATCGTGAGC 2076

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                                                                              640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for detecting
                                                                                                                                                                                                                                                                     GluThrLy81leGlyLy8AlaGlyTyrValThrAspArgGlyArgGlnLy81leValSer
                                      CTGACCGAGACCACCAGCAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGAC
                                                          AGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCCATCATCCAGGCC
                                                                                                                                      SerGlySerGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAla
                                                                                                                                                                                           CAGCCCGACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAG
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87US-00038330.
91US-00656797.
92US-00988530.
93US-00154397.
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N-PSDB; AAV63467.
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Sequence 1002
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The present invention relates to a process for the selection of human immunodeficiency virus (HIV) subtype isolates for use in the development of a prophylactic and/or therapeutic pharmaceutical composition. The process involves selecting isolated virus or viruses with a high sequence identity to a consensus sequence and a phenotype which is associated with transmission for the particular HIV subtype. The composition can be used in the production of vaccines against HIV. The present sequence is the HIV-1 subtype C isolate Dul51 pol protein. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selecting HIV-1 subtype C isolates, which are useful in developing vaccines against HIV infection, comprises isolating viruses with high sequence identity to a consensus sequence whose phenotype is associated with the HIV subtype.
                                          CAGATCGACAAGCTGGTGAGGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
                                AAGAAGGAGAAGGTGTACCTGAGCTGGCCCGCCCCACAAGGGCATCGGCGGCAACGAG
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                    Novel synthetic therapeutic peptide compounds useful for inducing a immune response in a mammal, specifically cross-react with HIV IV9 epitopes.
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Nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles, useful in immunizing a subject against HIV infection.
                                     viral particle; immunization.
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                                      promoter;
                        HIV protein for anti-HIV vaccine
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                                                   immunodeficiency virus
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                                      anti-HIV; vaccine; HIV;
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The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a nucleic acid used in the invention.
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Disclosure; SEQ ID NO 27; 166pp; English
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DEAV EL I (AAN80436) and LAV MA L (AAN80437) were isolated from the peripheral blood lymphocytes of patients. Different AIDS virus isolates concerned are designated by 3 letters of the patients name. Stable probes including the DNA sequences can be used for detection of the new LAV viruses or related viruses or DNA proviruses in eg. biological samples. The proteins or peptides can be used for detection of antibodies induced in vivo and present in biological fluids. The DNA can also be used for the expression of LAV viral antigens for the prodn. Of a vaccine against the detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct PI
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The specification describes a method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a substitutions. The method comprises typing all individuals of a complete of patients infected with a microorganism for at least one selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit or viruses and virus-like particles; for examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the hepatitis related viruses such as HCV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism or the drug affects the replication of the microorganism at the nucleotide or amino acid level. The present sequence represents a HIV pole protein, which is expected to provide optimal cytotoxic Tlymphocyte (CLL) induced therapeutic protection to the cohort examined in that study
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAG
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Matches:
Conservative:
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96.26%
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77.07%
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Claim 22; Page 88-89; 157pp; English

roValPheAlaIleLysLys 220 AGCTGAACAAGCGCACCCAG 927	CCTGGACGACGACTTCCGC 1047 :::	CTTCCAGAGCACATGACC 1167	CGCCAAGATCGAGGAGCTG 1287	GACCGTGCACCCATCGAG 1407	GTGCAAGCTGCTGCGCGC 1527	CGACCCCAGCAAGGACCTG 1647	CGCCCACACCAACGTG 1767	GACCTGGTGGACCGACTAC 1887
101 LyslleSerLyslleGlyProGluAsnProTyrAsnThrProValPheAlalleLysLys 868 AAGGACAGCACGAGGTGGACTTCCGCGAGCTGAACAAGCGCACCAG	988 GTGACCGTGCTGGACGTGGGCGACTTCAGCGTGCCCCTGGACGACGACGACGACGCCCTGGACGACGACGACGACGACGACGACGACGACGACGACGAC	108 TACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCATGACCAGAGCAGCATGACCAGAGCAGCATGACCAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	228 GACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGGCTG	348 CCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCGAG [468 TGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGCAAGCTGCTGCGCGGCCCAGCTGTGCTGCGCGGCGCGCGC	588 PACCGCGAGATCCTGCGCGGCCCGTGCACCGCGTGTACTACGACCCCAGCAAGGACTG	108 TTChAGAACCTGAAGAACGGCCAAGATGCGCACGCCCACACCACGACGTG	28 ACCCCCAAGTTCCGCCTGCCCATCCAGAAGAGACACTGGGGAGACCTGGTGGACCGACTAC 4

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HIV isola
HIV pol p
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Coden opt
Corrected
Lymphaden
HTV-1 pol
HTV-1 II
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Amino aci
HTV-1 pol
Wild type
AcNPV-HIV
HTV-1 pol
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HTV-1 pol
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HTV-1 non
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Sequence
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HIV-1 pol
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Aaw72993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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AAY70600
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 Anson D,
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LIMBERIS M.
FULLER M.
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    Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlh
-O=/cgn2 1/USFTO spool/US096.10313/runat 31052005 155136 15139/app_guery.fasta_1.7893
-O=/cgn2 1/USFTO spool/US096.10313/runat 31052005 155136 15139/app_guery.fasta_1.7893
-DB=A Geneseq 16Deco4 -OFWT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -SND=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-UNITS=bits -START=1 -SND=-1 -HEAPSIZE=500 -MINLENSO -MAXLEN=200000000
-USER=LOCAL_OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLENSO -NOFU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ads19486 Modified
Adp84803 HIV-1 hyb
Adn36406 Human pro
Aab69289 HIV-1 non
                                                                                              June 1, 2005, 11:33:41; Search time 167.833 Seconds (without alignments) 11351.628 Million cell updates/sec
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                                                                                                                                                                                      2463
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                    protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                of hits satisfying chosen parameters:
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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3766.5 3744.5 3711.5 3620 3611 3606 3570 3563 3571 3563

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Minimum DB seq Maximum DB seq

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Perfect score:

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Scoring table:

WPI; 2004-191004/18. N-PSDB; ADS19485.

Delivering exogenous (e.g. CFTR) genes to epithelial cells in the respiratory tract using a penetration agent and a lentiviral packaging system, useful for treating e.g. cystic fibrosis.

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Disclosure; Fig 16; 45pp; English

could are an unit of the degenerative mucleotide changes in the frame shift sequence AUGUDU to reduce the chance of a frame shift which switches expression of the Gappol protein to the Gap protein in the which switches capression of the cappol protein to the Gap protein in the which switches lentivirus. The exogenous gene is expressed in sufficient numbers of cells and amounts to provide an ameliorating effect for a respiratory condition. The exogenous gene is cystic fibrosis transmembrane conductance regulator (CFTR) and the condition is cystic fibrosis ((CF) the expression of the CFTR gene is sufficient to provide a significant shift of a reduced deltapD (transepithelial potential difference) back to normal levels in the mammal). The cell is non-cterminally differentiated and is capable of differentiating into 2 or more cell classes e.g. ciliated cells, non-ciliated cells, secretory cells and basal cells. The exogenous gene may be enzymic. The gappol gene sequence has additionally degenerate nucleotide substitutions which destabilise the hairpin structure associated with the frame shift event. The gag gene is a truncation of the wild type gappol gene so that it can no longer be translated to form Gappol. The lentivirus is HIV or HIV derived. The method and recombinant lentiviral packaging system may be used for delivering nucleic acids to epithelial cells in the respiratory cued for delivering nucleic acids to epithelial cells in the respiratory The present invention relates to a method of delivering one or more exogenous genes for expression in an epithelial cell in the respiratory system of a mammal to give persistent expression of the gene in the epithelial cell, using a lentivital packaging (expression vector) system. Also disclosed are (i) a recombinant lentivital packaging system. Comprising a first nucleic acid molecule including a gag gene sequence encoding a GagPol protein (the gagpol gene sequence encoding a GagPol protein (the gagpol gene sequence has degenerative nucleotide changes in the frame shift sequence AUTUVUV to reduce the chance of a frame shift which switches expression of the Gagpol protein to the Gag protein in wild type lentivirus and the gagpol protein to the Gag protein in wild type lentivirus and the molecule which does not encode either the gag gene or the gagpol gene or combinant and (ii) a recombinant nucleic acid molecule encoding a lentiviral system of a mammal. In particular they may be used to deliver the CFTR gene for the treatment of CF. It has been found that the delivery of a recombinant lentivirus carrying an exogenous gene to the respiratory system, following the delivery of a non-toxic amount of a penetration enhancer can provide persistence of expression of a gene product. The present sequence represents modified HIV-1 GagPol protein.

Sequence 1435 AA;

Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-610-313B-31 (1-2463) x ADS19486 (1-1435) Gaps: 2.87e-209 3766.50 94.31% 88.75% 82.36% Score:
Percent Similarity: Alignment Scores: Query Match: DB: 엄 ð

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mammal an immune response directed to a virus, preferably Human

mammal an immune response directed to a virus, preferably Human

mammal an immune response directed to a virus, preferably Human

mammal an immune response directed to a virus, preferably Human

muncheic acid molecules mooding all, part or a modified form of two

cor more antigens of the virus are incorporated, and one or more optimized

cor more antigens of the virus are incorporated, and one or more optimized

cor more antigens of the virus are incorporated, and one or more optimized

cor more incorporated and one or more optimized

cor more incorporated in a mammal, a method of vaccinating or

preventing viral infection in a mammal; a vaccine capable of inducing an

immune response directed to a virus comprising the recombinant plasmid

vector or recombinant viral vector or its functional derivative; a

concleic acid construct or its functional derivative; a

concleic acid construct or its functional derivative; a

concleic acid construct or its functional derivative; a

recombinant viral vector; a pharmaceutical composition comprising the

combinant viral vector or recombinant viral vector constructs. The

method is useful in eliciting or inducing in a mammal an immune response

adainst HIV-1 subvype AE, B Dx C. This sequence represents the protein of

the HIV-1 hybrid isolate pNL4-3 DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eliciting or inducing in a mammal an immune response against HIV-I subtype AE, B or C by administering sequential doses of a recombinant plasmid and viral vectors containing the nucleic acid molecules encoding the HIV antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramshaw IA;
                                                                                                                                                                                                                                                          response; HIV; antigen; non-pathogenic;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                       HIV-1 hybrid isolate pNL4-3 protein.
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ADP84803 standard; protein; 3183
                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
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17-SEP-2003; 2003AU-00905067.
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3744.50
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82.31%
81.88%
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                                                                                                                                                                                                                                                          eliciting; inducing; immune vaccination; vaccine; HIV-I.
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Pred. No.:
                                                                                                                           23-SEP-2004
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                                                                  ADP84803;
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(1-3183)

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                     AspSerGlyLeuGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGln 1162
                                                                                                                   AAGGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAG
                                                                                                                                               The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a peptide used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles, useful in immunizing a subject against HIV infection.
                                                                                                                                                                     ATCGACAAGCTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2364
                                                                                                                                                                           GCCCAGCCCGACAAGAGCGAGAGCGAGAGTGAACCAGATCATCATCATCAAG
                      GACAGCGCCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAG
                               HIV; promoter; viral particle; immunization.
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                                                                                                                                                                                                                                                         Human protein for anti-HIV vaccine
                                                                                                                                                                                                               standard; protein; 1457
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N-PSDB; ADN36405.
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Length: Matches:

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Alignment Scores:

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                                                                                                            AAGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGCCACATCGCCGC
                                                                                                                                                                                                                   AAGGACTGCACCGAGCCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGC
                                                                                                                                                                                                                                                                            AAGGCCCGCGAGTTCCCCAGCGAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTG
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                                                                                            ATGCCCAGGCCATGAGCCAGGCCACCAGCCCAACATCCTGATGCAGCGCAGCCAACTTC
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 28
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21
4
Conservative:
Mismatches:
Indels:
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91.86%
88.36%
81.16%
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The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                  rLeuThrGluThrThrAsnGlnLysThrGluLeuGlnAlaIleCysLeuAlaLeuGlnAs
                                                                                                                  GGAGAAGGTGTACCTGAGCTGGGTGCCCGCCCACAAGGGCATCGGCGGCAACGAGCAGAT
                                                                                                                             CAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGC
                                                    CCAGCCCGACAAGAGCGAGAGCGGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA
                                                                                         aGlnProAspLysSerGluSerGluLeuValAsnGlnIleIleGluGlnLeulleLysLy
                                                                                                                                                              Novel genomic nucleic acids of non-subtype B human immunodeficiency type 1 useful for detecting and treating AIDS comprises a specific
                                                                                                                                                     CGACAAGCTGGTGAGCCAAGGCCAAGGTGCTGTTCCTGGACGGCATCGAT
                                                                                                                                                                                                                                                                                        pol;
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                                                                                                                                                                                                                                                                                        non-subtype B;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                         immunodeficiency virus;
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                                                                                                                                                                                                                                                                                                 vif; vpr; tat; rev; nef; vaccine.
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3620.00
98.05%
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(first entry)
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nucleotide sequence.
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Best Local Similarity:
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20-APR-2001
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                                                                                                                                                                                                          env; vpu;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B; gag; pol; env; vpu;
                       AAGACCGGCAAGTACGCCAAGATGCGCACCCCCACACCAACGACGTGAAGCAGCTGAACC
                                                                                                                                                     ACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATC
                                              CTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATC
                                                      CAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTG
                                                                                       GlnLysGlnGlyHisAspGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeu
                                                                                                                     GAGGCCGTGCAGAAGATCGCCATGGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTC
                                                                                                                                                                            CGCCTGCCCATCCAGAAGGAGCCTGGGAGACCTGGTGGACTACTGGCAGGCCACC
                                                                                                                                                                                    TGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGGTGAAGCTGTGGTACCAGCTG
                                                                                                                                                                                                                                            GAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAG
                                                                                                                                                                                                                                                                                                                                                  GlySerGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaHis
                                                                                                                                                                                                                                                                                                                                                                                 ProAspLysSerGluSerGluLeuValAsnGlnIleIleGluGlnLeuIleLysLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV-1; human immunodeficiency virus; non-subtype vif; vpr; tat; rev; nef; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-subtype B clone 96ZM751-3 pol protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB69287 standard; protein; 1005 AA.
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Human immunodeficiency virus 1.

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                                                                                                                                                                                                                                                                     The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IleThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlnIleLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCACCCTGTGGCGCCCCCCTGGTGAGCATCAAGGTGGGCGCCCAGATCAAGGAGGCC
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                                                                                                                                                                       of non-subtype B human immunodeficiency and treating AIDS comprises a specific
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                                                                                                                                                                                                                                          Claim 41; Fig 15; 131pp; English.
99WO-US024837
                              98US-00184418
                                                                                                                                                                       Novel genomic nucleic acids
type 1 useful for detecting
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96.68%
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                                                                                                                                                                                                           nucleotide sequence.
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Best Local Similarity:
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The invention relates to molecules comprising HIV-1 subtype isolate regulatory/accessory genes (tat. nef and rev genes) and modifications and derivatives thereof. The invention also provides proteins encoded by such genes. Sequences of the invention are useful for manufacturing vaccines for treating or preventing human immunodeficiency virus (HIV) infections. They are also useful in gene therapy. The present sequence is HIV-1 subtype C isolate Dui51 reverse transcriptase (RT) protein. (Updated on 23-0CT-2003 to standardise OS field)
                                             New molecules comprising HIV-1 subtype isolate regulatory/accessory genes, useful for manufacturing a vaccine for treating or preventing HIV infection.
                                                                                                                                                        Disclosure; Page 94-97; 97pp; English.
WPI; 2003-430497/40.
N-PSDB; AAD29258.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 998 AA;
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Alignment Scores: Pred. No.:	6.01e-198	Length:	866
Score:	3570.00	Matches:	999
Percent Similarity:	97.07	Conservative:	29
Best Local Similarity:	93.02\$	Mismatches:	19
Query Match:	78.078	Indels:	2
DB:	9	Gaps:	1
US-09-610-313B-31 (1-2463) x AAE37601 (1-998)	63) x AAE37601	(1-998)	
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S G	523 p	ATCGGCGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAG 582 	82
oy Pb	583 A	AAGGCCATCGCCCCCGTGAACCACCCCCGTGAACATCATCGGCCGCAACATG 642	2 4 6
Oy 6 Db 1	643 C	CTGACCCAGCTGGGCTGCACCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCGTG 702	20 09
Oy 7	703 A 161 L	AAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAG 762 	80
φ, 1	763 A 181	ATCAAGGCCCTGACCGCCATCTGCGAGGACATGGAGGAGGGGGGAGGATCACCAAGATC 822	2. 0
Oy E	823 G 201 G	GGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAG 882	2 3

88 100 100 100 100 100 100 100 1	3 TGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACCAGCGCACCCAGGACTTCTGGGAGGTG 942	3 CAGCTGGGCATCCCCACCCGCCGGCCTGAAGAAGAAGAAGAGGTGGTGCTG 	3 GIGGGCGACGCCTACTICAGCGTGCCCCTGGACGACTTCCGCAAGTACACCGCCTTC 1062 	063 ACCATCCCCAGCATCAACAACGAGCACCCCGGCATCCGCTACCAGTACAACGTGCTGCCC 1122 	3 CAGGGCTGGAAGGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCC 1182	3 TTCGGGGCCGGAACCCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGC 1236	7 AGGACCTGGAGATCGGCCAGCACGCGCCAAGATCGAGGAGCTGCGCAGGCACCTGCTG 1296	7 CGCTGGGGCTTCACCCCCCGACAAGAAGCACCA :::	7 GGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCGGAG7 	7 AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAACTGAACTGGGCCAGCCA	7	7 GACATCGTG 1 Aspileval	CGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAG 1 :::	7 AAGCAGGGC	7 ACCGGCAAG 1 ThrGlyLys	7 1	carccagaaggagaccrgggaggcggggggggggggggg	7 ATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCTGGTGAAGCTGTGGTACC
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induction of specific humoral and cellular immune responses. (I) and polypeptides (II) encoded by them, are useful in pharmaceuticals, waccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virtue-1 (HIV-1) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in the method of the invention. (Updated on 11-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTG-----CGCGGCGACAACCCCCGCAGCCGGCGCCCGAGCGCCAAGGCCACCCT
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                                                                                                                                                                                        SerGluValAsnIleIleThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaGlnPro
                                                                                                                                                                                                                                                                                                                                GACAAGAGCGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAG
                                                                                                                                                                                                                                                                                                                                                     AspargSerGluSerGluLeuValAsnGlnIleIleGluGlnLeuIleLysLysGluArg
                                                                                                                                                                                                                                                                                                                                                                                                           AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACC
                                                                                                                                                                   GAGACCACCAGCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGC
                                                                                                                                                                                                                                                  AGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; diagnosis; human; humoral immune response; antiviral; immune response; vaccine; treatment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTGAGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
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1. .3025
/label= Xaa
/note= "Xaa represents a
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ACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGG
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                   Claim 41; Fig 15; 131pp; English
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3517.50
95.96%
91.92%
76.92%
                                 present in invention
       nucleotide sequence.
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Best Local Similarity:
Query Match:
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useful
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                                              nGluProPheLysAsnLeuLysThrGlyLysTyrAlaLysArgArgThrThrHisThrAs
             CGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGACCATCGTGATCTG
                    GGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGAC
                                                                  rAspTyrTrpGlnAlaThrTrpIleProGluTrpGluPheValAsnThrProProLeuVa
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                                                                                                            number of human immunodeficiency virus (HIV) type 1 non-subtype B stolates. The sequences shown include the near full-length coding sequences from each isolate, and the env. pol, vif. vpr. vpu. gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies gainst non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                          provides the protein and coding sequences
for detecting and treating AIDS comprises a specific
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GAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCGCGCAGAAGATCGTGAGC
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87US-00038330.
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13-APR-1987;
19-FEB-1991;
10-DEC-1992;
18-NOV-1993;
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CC antigens are also useful in vaccines. (Updated on 25-WAR-2003 to correct XXX Squares 102 AA; Alignment Scores: 1	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1111 TyrThrAlaPheThrIleProSerIleAsnAsnGluThrProGly1leArgTyrGlnTyr 300 1111 AACGTGCTGCCCGGGGCTGGAAGGGGCGCCCGGATTTCCGAGGCGGGGGGGG
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                                                                                                                                                                                              Human immunodeficiency virus; HIV; pol; IV9; immunotherapy; infection;
                                                   CAGATCGACAAGCTGAGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGCCATCGAT
                                                                                    TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAAGGCCCGCGAGTTCCCCCAGCGAGCAG
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                                                                                                                                                                                                                                                                                                                                                      Novel synthetic therapeutic peptide compounds useful for inducing a immune response in a mammal, specifically cross-react with HIV IV9 epitopes.
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immunization

viral particle;

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for anti-HIV vaccine
                                    Human immunodeficiency virus
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                           anti-HIV; vaccine; HIV;
                                             WO2004035006-A2
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The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a nucleic acid used in the invention.
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                                                                                                                                                      Nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles, useful in immunizing a subject against HIV infection.
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Indels:
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18-OCT-2002; 2002US-0419465P
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                                                                  Huang Y, Ho DD, Chen Z;
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N-PSDB; ADN36412.
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ADN36413 standard; protein; 1003

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LAV EL I (AAN80436) and LAV MA L (AAN80437) were isolated LICUM LUE peripheral blood lymphocytes of patients. Different AIDS virus isolates concerned are designated by 3 letters of the patients name. Stable probes including the DNA sequences can be used for detection of the new LAV viruses or related viruses on DNA proviruses in eq. biological samples. The proteins or peptides can be used for detection of antibodies induced in vivo and present in biological fluids. The DNA can also be used for the expression of LAV viral antigens for the prodn. of a vaccine against LAV. The polypeptides can also be used for the prodn. of antibodies for the detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                   New variants of lymphadenopathy associated virus (LAV) - used for prodn. of DNA, antigens and antibodies used in diagnosis of AIDS and pre-AIDS.
                                                                                Alizon M;
                                                                          Wainhobson S, Montagnier L, S, Montagnier L;
                                                                                                                                                                                                                                                              Claim 8; Fig 8A-8I; 72pp; English
86EP-00401380
                                                                            Sonigo P, Wainhobson
                                      (INSP ) INST PASTEUR
                                                                                                                                       WPI; 1988-014396/02.
N-PSDB; AAN80437.
23-JUN-1986;
                                                                            Alizon M,
Sonigo P,
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1002 652 39 24 5 Length:
Matches:
Conservative:
Mismatches:
Indels: 1.39e-193 3494.50 95.97% 90.56% 76.42% Percent Similarity: Best Local Similarity: Sequence 1002 AA Alignment Scores: Query Match:

TGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGCCAGGATCAAGGAGGCCCTGCTGGAC 450 ACCEGCECCANCANCACTECTGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAG 510 ATGATCGGCGGCGATCGGCGCGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAG 570 ATCTGCGGCAAGAAGGCCATCGGCACCGTGATCGGCCCCCACCCCCGTGAACATCATC 630 GGCCGCAACATGCTGACCCCAGCTGGGCTGCACCCTGAACTTCCCCCATCAGCCCCATCGAG 690 ITCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCCAGCGAGCAG 279 AACCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTG----CGCGGCGACAACCCCCGGC 336 AGCGAGGCCGCCGCCGAGCGCCAGGGC----ACCCTGAACTTCCCCCAGATCACCCTG 390 (1-1002)US-09-610-313B-31 (1-2463) x AAP81861 21 280 337 41 391 61 451 81 511 101 571 121 631 g 셤 셤 8 8 셤 ò ద 셤 8 ઠે 8 ઠે Š ሯ

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CACCAAG eLeuLys
CAGCACC pSerThr
CTGGGAG eTrpGlu
CGTGCTG rValleu
CACCGCC rThrAlal
111 AACGTGCTGCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAG 117
CCTGGAG(eLeuGlu
GTACGTGC
GCACCTGC : uHisLeuL
CCTGTGGA eLeuTrpM
CGAGAAGC ::: oAsplysC
CAGCCAGA aSerGlnI
.GGCCCTG2 BAlaLeu1
CGAGATCC gGluileI
CGAGATCC aGluIleC
GAACCTG
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GlnLeuThrGluAlaValGlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThr
                           | TACCAGCTGGAGAAGAAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGCC
                                                                                                       GInAspSerGlySerGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIle
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                                                                                                                                                                                                                                                                                               CCCAAGTTCCGCCTGCCCATCCAGAAGGAGCCTGGGAGCCTGGTGGACCGACTACTGG
                                                        GTGAGCCTGACCGAGACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTG
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                                                                                                                                                                                                                                                                                                                         CAGATCGACAAGCTGGTGAGCAAGGCCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic marker; host response; HIV; AIDS related virus; vaccine; hepatitis related virus; HCV; HBV; drug resistance; pol.
                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of a HIV pol protein.
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                                                                                                                                                                                                                                                                                                                                                                                 ABR55489 standard; protein; 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2001; 2001AU-00008425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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The specification describes a method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a population of patients infected with a microorganism for at least one selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit pathogenic traits in a host, such as bacteria, fungl, mycobacterium, viruses and virus-like particles; for examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the hepatitis related viruses such as HV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistance in patients treated with a particular drug specific for a microorganism check muchecide or amino acid level. The presents at the nucleotide or amino acid level. The present sequence represents a HIV pol protein, which is expected to provide optimal cytotoxic I lymphocyte. CTL) induced therapeutic protection to the cohort examined in that study

Sequence 1003 AA;

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                                                                                                                      TTCTTCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAG
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Claim 22; Page 88-89; 157pp; English

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A;Accession: 554378
A;Status: preliminary
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Roses: 1-1002 <THE>
A;Cross-references: UNIPROT:P12499; EMBL:M22639; NID:g329377; PIDN:AAA45366.1; PID:g3293
C;Superfamily: pol polyprotein
C;Keywords: polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pol polyprotein - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCGCGCCAACAGCCCCCACCAGCCGCGAGCTGCAGGTGCGCGC---GACAACCCCCGC
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-MODEL=frame+ n2p.model -DEV=xlh
-Q=/Cogn_21/USPTO_spool/USO9610313/runat_31052005_155137_15159/app_query.fasta_1.7893
-Q=/Cogn_21/USPTO_spool/USO9610313/runat_31052005_155137_15159/app_query.fasta_1.7893
-DE-PIR 79 -QFMT=fastan -SUFPIX=h2p.rpr -MINNATCH=0.1 -LOOPCIX=0 -LOOPEXT=0
-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=Dits -START=1 -END=-1 -MATRIX=DO -TIR MIN=0 -ALIGN=15 -MODE=LOCAL
-OURTENT=pto -NORM=ext -HEAFSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=USO9610313_@CGN 1 1_189_@runat_31052005_155137_15159 -NCPU=6 -ICPU=3
-NO_WARA P-LARREGOUERY -NEG SCORES=0 -WAIT -DSPBLOKE=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDST=7
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                                                                                                                                                                                                          gtcgacgccaccatggccga......gggctagcaccggtgaattc 2463
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                              protein search, using frame_plus_n2p model
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Database

Total number

Searched:

336

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Result

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Oy 1465 GCCAGCCAGATCTAC	Db 461 ArgGluIleLeuLy, Qy 1645 GCCGAGATCCAGAA Db 481 AlaGluIleGlnLy, Qy 1705 AAGAACCTGAAGAC	501 1765 521 1825	Db 541 ProLysPheArgLel Qy 1885 CAGGCCACCTGGATC Db 561 GlnAlaThrTrpIl Qy 1945 TACCAGCTGAAAA	Db 581 TyrGlnLeuGluLyy Oy 2005 AACCGCGAGACCAA Db 601 ASTAIGEITHIIII Oy 2065 GTGAGCCTGACCAA	621 2125 641 2185		RESULT 2 GNLJND HIV-1 retropepsin (EC 3.4.23 NiContains: endonuclease (EC C;Species: human immunodefic A;Note: host Homo sapiens (m. C;Date: 30-Sep-1991 #sequenc C;Accession: J0067 R;Spire, B.; Sire, J.; Zacha Gene 81, 275-284, 1989 A;Title: Nucleotide sequence A;Reference number: J00065; lA;Accession: J00067
TGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC [101 ATGATCGGCGGCATTCGGCGGCTTCATCGAGGTGCGCCGGTGGGGGGGG	631 GGCCGCAACATGCTGACCCAGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAG 690 141 GlyArgAsnLeuThrGlnIleGlyCysThrLeuAsnPheProIleSerProIleGlu 160 691 ACCGTGCCCGTGAAGCCCGCATGGACGCCCCCAGGTGAAGCAGTGACCCCTG 750 [751 ACCARGARANGATTCARGGCCCTGACCGCCATCTGCGAGGGAGGAGGAGGGGGGGGG	871 GACAGCACCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGAC 930 221 AspSerThrLysTrpArgLysLeuValaspPheArgGluLeuAsnLysArgThrGlnAsp 240 231 TTCTGGGAGGTGCAGCTGGGCATCCCCCCCGCCGCGCCTGAAGAAGAAGAAGAGGGTG 990 231 TTCTGGGAGGTGCAGCTGGGCATCCCCCCCCCCCGCCGCTGAAGAAGAAGAAGAAGGGTG 990 241 PheTrpGluValGlnLeuGlyIleProHisProAlaGlyLeuLysLysLysLysSerVal 260	ACCGTGCTGGACGTGGGCGACGCCTACTTCAGGTGCCCCTGGACGAGGACTTCCGCAAG	1111 AACGTGCCCAGGGCTGGAAGGCAGCCCACATTCCAGAGCACATGACCAAG 1170 301 ASNValleuProGlnGlyTrpLysGlySerProAlailePheGlnSerSerMetThrLys 320 1171 ATCCTGGAGCCCTTCGGCCCGCAACCCGGAGTCGTGATCTACCAGGCCCC 1224	341 LeufyrvaldlySerAspLeudluiledlydlnHisArgThrLysiledludluLeuArg 360 1285 AAGCACCTGCTGCGCTGGGGCTTCACCACCCCGACAGAAGCACCAGAAGGACCCCCC 1344 :::
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                                 ACATCGTGCCCCTGACCGAGGCCGAGCTGGAGCTGGCCGAGAAC
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GNLJND HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate NDK) N,Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polym C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004 C;Accession: JQ0067 R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.; lene 81, 275-284, 1989 1,Title: Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immunoc Ysfeference number: JQ0065; MUID:90034200; PMID:2806917

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AAGCACCTGCTGCGCTTGAGCACCCCCCGACAAGAAGCACCAGAAGGAGCCCCCCC 1344
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A; Molecule type: DNA
A; Residues: 1-1002 <SBI>
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A; Residues: 1-1002 <SBI>
Cross=references: UNIPROT: P18802; GB: M27323; NID: g328154; PIDN: AAA44869.1; PID: g328158
C; Croment: Specific enzymatic cleavages may yield mature proteins including protease, re
C; Genetics:
A; Genetics:
C; Superfamily: pol polyprotein
C; Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nuclec
F; 56-154/Product: retropepsin #status predicted <RTP>
F; 86-154/Product: Asp (shared with dimeric partner) #status predicted
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qa	461 AsnArgGlulleLeuLysGluProValHisGlyValTyrTyrAspProSerLysAspLeu 480	A; Gene: pol
è a	1642 GTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCC 1701 	C.Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo. F;69-167/Product: retropepsin #status predicted <rtp> F;69-167/Product: ABP (shared with dimeric partner) #status experimental</rtp>
è 4	1702 TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCCAACGACGTG 1761 	6.73e-154 Length: 3475.00 Matches:
<i>ት</i> 8	1762 AAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG 1821 	reform Similarity: 93.7.4 Conservative: 33 Best Local Similarity: 89.22\$ Mismatches: 28 Query Match: 15.99\$ Indels: 18 DB: 1
È i	ACCCCAAGITCCGCCTGCCCATCCAAAGGAAACTGGGAACCTGGGACCGACTAC	-09-610-313B-31 (1-2463) x GNVWH3 (1-1015)
8 &	541 ThrProLysPheLysLeuProlleGlnLysGluThrTrpGluThrTrpTrpThrGluTyr 560 1882 TGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCC	<pre>Qy 220 TICTICCGGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTIC 267 </pre>
요 ?	561 TrpGlnAlaThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeu 580	Qy 268CCCAGCGAGCAGAACCGCGCCAACAGC 303
2 A		304 CGCGAGCTGCAGGTGCGCGGCGAGCCCCCCGCAGCGAGCGGCGGCGGCGGCGGCG
දු දු	2002 GCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGGGGCCGGCAGAGG 2061 :::	Db 41 ArgelüLeüGinValTrpGlyArgAspAsnAsnAsserProSerGiùAlaGlyAlaAspArg 60 Qy 358 CAGGGCACCCTGAACTTCCCCCAGATCACCCTGTGGCAGCGCCCCTGGTGAGC 411
ò	ATCGTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCC	
음 &	621 ValValThrLeuThrAspThrThrAsnGlnLysThrGluLeuGlnAlaileHisLeuAla 640 2122 CTGCAGGACAGCGAGGTGAACATCGTGACCGACAGCCAGTACGTCGTGGCCTTGGGCATC 2181	Oy 412 ATCAAGTGGGGGCCAATCAAGAGGCCTGGTGGACACCGGGCGCGACCACCGTG 471 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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රු සි	2182 ATCCAGGCCCAGCCCGACAAGAGCGAGCGAGCTGGACCAGATCATCGAGCAGCTG 2241	Db 101 LeuGluGluMetSerLeuProGlyArgTrpLysProLysMetileGlyGlylleGlyGly 120 Ov 532 TTCATCAAGGTGCGCCAGTACGACGATCGAGATCTGAGATCTGCGGCAAGAAGGCCATC 591
è	ATCAAGAAGAAGGTGTGGCTGGGTGGCCGCCAACAAGGGCATCGGCGAAC	121 PheileLysValArgGlnTyrAspGlnIleLeuileGluileCysGlyHisLysAlaile 1
음 6	681 IleLysLysGluLysValTyrLeuAlaTrpValProAlaHisLysGlylleGlyGlyAsn 700 2302 GAGCAGATCGACAAGGGAAGGGAAGGTCCGGAAGGTCCTGTATCTGACGACGATCAAGGGAAGGTCCGGAAGGTCTGTTCCTGGAAGGGATC	Qy 592 GGCACCGGCGTGATCGGCCCCAGGAGACATCATCGGCCGCAACATGCTGACCCAG 651
6 음	:::	652 CTGGGCTGCACCCTGAACTTCCCCCATCGACCCCATCGACACCGTGCCCGTGAAGGTGAAGG
8 1	GAT 2	161 116GlyCysThrLeuAsnPheProlleSerProlleGluThrValProValLysLeuLys
DD RESULT	721 Asp 721 4	<pre>Qy 712 CCCGGCATGGACGCCCCCAAGGTGAAGCACTGGCCTGACCGAGGAGAAGATCAAGGCC 771 </pre>
HIV-1 1 1 Conte	retropepsin (BC 3.4.23.16) - human immunodeficiency virus type 1 (isolate HTLV-III ains: endonuclease (BC 3.1); retropepsin (BC 3.4.23.16); RNA-directed DNA polyies: human immunodeficiency virus type 1, HIV-1	Oy 772 CTGACCGCCATCTGCGAGGAGATGGAGGGCCAAGATCACCAAGATCGCCCCGGG 831
A; Note C; Date C; Acce R; Ratn	A;Note: now Homo Saptens (man) C;Date: 108 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03965 R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora	Oy 832 AACCCCTACAACACCCCGTGTTCGCCATCAAGAAGAAGAACAGCACCAAGTGGCGCAAG 891
Nature A;Titl(A;Refer	1, 3.77-284, 1985 13. 3.77-284, 1985 13. Complete nucleotide sequence of the AIDS virus, HTLV-III. rence number: A93353; MUID:85111123; PMID:2578615	Qy 892 CTGGTGGACTTCCGCGAGGTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGCGC 951
A; Molec A; Molec A; Resic	Beach : AUSPos culle type: DNA lues: 1-1015 - RRAT.	952 ATCCCCACCCGCCGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGACGTCGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTACACACAC
A;Crosi C;Comm(C;Genet	B-references: UNIPRUT:P03366; GB:R15654; GB:RUZUUB; GB:RUZUUB; GB:RUZUUB; NID:g328 ent: Specific enzymatic cleavages may yield mature proteins including protease, re tics:	DD Z61 11eFrOH18FrOA18G1yLeULy8Ly8Ly8Ly8Ly8LAILNIYVAILEUABPVAIG1yA8D Z80 Qy 1012 GCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC 1071

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TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCCCCCACACCAACGACGTG
      1822 ACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCTAC
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RESULT 6

H44001

H17-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (strain YU-2)

H17-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1)

N;Contains: endonuclease (EC 3.1....); retropepsin (EC 3.4.23.16); RNA-directed DNA poly.

C;Species: human immunodeficiency virus type 1, H1V-1

A;Note: host Homo sapiens (man)

C;Accession: B44001

R;Li, Y; Hui, H; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Reference Type: DNA

A;Residues: 1-103 < LIY>

A;Residues: 1-103 < LIY>

A;Residues: 1-103 < LIY>

A;Cross=references: UNIPROT:P35963; GB:M93258

C;Comment: This protein is synthesized as a gag-pol polyprotein: including proteinse,

A,Gene: pol C,Superfamily: pol polyprotein C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo F,57-155/Product: retropepsin #status predicted <RTP> F;87-155/Active site: Asp (shared with dimeric partner) #status predicted

GGCGGCGAAC 2301	CATC 2361	748 CTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAC	DD 181 LeuinFGludAuLy81leLy8AlaLeuValGlulleCy8InFGLUM		M.M.; Brown-Sh Qy 928 rus (ARV-2). Db 241	.1; PID:93286	ng protea	mmunodeficiency; nucled Qy 1108 TACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCCCCAGCATTCCAGAGCAGCCAGC	1168	Qy 1222 CCCTGTACGTGGGCACCTGGACCTGGACATCGGCCAGCACCGCGCCAAGATCGAGATCTG	GCAG	uGln cccc	ASPIASINS		507 Qy 1522 507 Db 441	OV 1582 AACCGCGAGATCCTGCGCGAGCCCCGTGCACGCGTGTACTACGACCCCAGCAAGGACCTG
2242 ATCAAGAAGGAGAAGGTGTACCTGAGCTGGCCGCCCCACAAGGGCATCGGCG 	2302 GAGCAGATCGACAAGCTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGGC :::	2362 GAT 2364 721 Asp 721	RESULT 7 GNVWA2 HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus N;Contains: endonuclease (EC 3.1); retropepsin (EC 3.4.23.1	ecies: human immunodeficiency virus type 1, HIV-1 Le: host Homo sapiens (man) te: 17-May-1985 #sequence_revision 17-May-1985 #text_change cession: A03968	RiSanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, Science 277, 44-492, 1985 A;Title: Nucleotide sequence and expression of an AIDS-associated retrovi. A;Reference number: A04003; MUID:85090453; PMID:2578227	cession: A03968 lecule type: DNA sidues: 1-1003 «SAN» oss-references: UNIPROT:P03369; GB:K02007; NID:G328658; PID	mment: Specific enzymatic cleavages may yield mature protein netics: ne: pol perfamily: pol polyprotein	;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; ;57-147/Product: retropepsin #status predicted <rtp> ;81/Active site: Asp (shared with dimeric partner) #status pred</rtp>	Alignment Scores: 1.08e-152 Length: 1003 Pred. No.: 3449.00 Matches: 646 Percent Similarity: 94.87% Conservative: 38	89.60* Mismarches: 75.42* Indels: 1 Gaps:	US-09-610-313B-31 (1-2463) x GNVWA2 (1-1003) QY	1 PhePheArgGluAspLeuAlaPheLeuGlnGlyLysAlaArgGluPheSerSerGl 280 AACCGGGCGAACAGCCCACCAGCGGAGCTGCAGGTGCGGGGGGACAA	11 INTAFGALAABNSerProintArgArgGilleGusinValitpGilyGilyGilaBnAB 334 CGCAGCGAGCGGGCGAGCGCCAGGGCACCCTGAACTTCCCCCAGAT	41 LeussfoldataGlyataAsBpArgGlNGLYIMfValseffneAshnefflociniltelmi 388 CTGTGGCAGCGCCCCTGGTGAGCATCAAGGGCGCCAGATCAAGGAGGCCTGCTG [

Score: 3439.00 Matches: 647 Percent Similarity: 93.67% Conservative: 34 Best Local Similarity: 89.00% Mismatches: 28 Query Match: 75.20% Indels: 18 DB: 1 Gaps: 4 US-09-610-313B-31 (1-2463) x GNVWVL (1-1012) 4 4 Qy 238 GCCTTCCCCCAGGGCAAGGCCCGCAAGTTC	268CCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCGGGAGCTGCAGGGG 31	36 63	OY 370 AACTICCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAG 429	Qy 430 ATCAAGGACCCTGCTGGACACCGCCCACGACGACGAGGAGAGGACTGG 489 :::	Qy 490 CCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAG 549	Oy 550 TACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGC 609	Oy 610 CCCACCCCGTGAACATCATCGCCGCAACATGCTGACCCAGCTGGGCTGCACCTCAAC 669	Qy 670 TTCCCCATCAGCCCCATCAGACCTGCAGAACCTGAAGCCCGGCATGCACGCCCC 729 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 730 AAGGTGAAGCAGTGGCCCCTGACCGAGAGAGAGATCAAGGCCCTGACCGCCATCTGCGAG 789 	0y 790 GAGATGGAGAAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCC 849 Db 204 [
520 1921 1821 1881 6		2001 C	2061 Ç	2121 C	2181 6	2241 C	2301 C	2361 C		DNA poly D.J. retrovi ease, re , nuclec
1702 TTCAAGAACCTGAAGATACGCCAAGATGCGCACGCCCACACCACCAAGGTG 1702 TTCAAGAACCTGAAGATGCGCAAGATGCGCACCACCACCACCACCAAGATGTG 1	TGGCAGGCCACCTGGATCCCCGAGTGGGAACACCCCCCCC		2002 GCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACC	2062 ATCGTGAGCCTGACCGAGACCACCACCAGAGCCGAGCTGCAGGCCATCCAGCTGGCC 21 :::	2122 CTGCAGGACGGCAGCGAGGAGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATC 21	2182 ATCCAGGCCCACCACAAGAGGGAGGGAGGTGGTGAACCAGATCATGGAGGAGCTG 22	2242 ATCAAGAAGGAGAAGGTGTACCTGAGCTGGCTGCCCGCCACAAGGCCATCGGCGGCAAC 23	2302 GAGCAGATCGACAAGCTGGTGAGCAACCGCAAGGTGCTGTTCCTGGACGCATC 23	2362 GAT 2364 721 Asp 721	RESULT 8 GNVWVL HTV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate NIV-1 retropepsin (EC 3.4.23.16); RNA-directed C; Species: human immunodeficiency virus type 1, HIV-1 C; Accession: A03967 R; Mucesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon Nature 313, 450-458, 1985 A; Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy A; Reference number: A93155; MUID:85111157; PMID:2982104 A; Accession: A03967 A; Residues: 1-1012 < MUE> A; Residues: UNIPROT:P03368 C; Comment: Specific enzymatic cleavages may yield mature proteins including prot C; Genetics: A; Gene: pol C; Superfamily: pol polyprotein C; Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency F; 66-164/Product: retropepsin #status predicted < RTP> F; 90/Active site: Asp (shared with dimeric partner) #status experimental Alignment Scores: A; Pred. No.: S114e-152 Length: 1012

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HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus SIVcpz
N;Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
S;Species: simian immunodeficiency virus SIVcpz
N;Contains: endonuclease (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
S;Species: simian immunodeficiency virus SIVcpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
R;Huer, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: 809983; MUID:90259077; PMID:2188136
A;Accession: 809984
A;Status: nucleic acid sequence not shown; translation not shown
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C;Superfamily: pol sapartic proteinase; endonuclease; hydrolase; immunodeficiency;
C;R-1-180/Product: retropepain #status predicted <RTP>
F;81-180/Active site: Asp (shared with dimeric partner) #status predicted
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                                              AAGGGCATCGGCGCCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTG
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A.Residues: 1-1027 «HUE»
A.Cross-references: UNIPROT: P17283; EMBL: X52154
C.Gomment: Specific enzymatic cleavages may yield mature
A.Genetics:
A.Gene: pol
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Conservative:
Mismatches:
Indels:
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91.11%
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Best Local Similarity:
Query Match:
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EMBL:Z11530; NID:g60192; PIDN:CAA77622.1; PID:g60194
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533980
pol polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33880
R;Carlini, F:
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Reference number: S33979
A;Reference number: S33980
A;Reference number: J-192
A;Accession: S33980
A;Residues: 1-912 < CAR>
A;Residues: 1-912 < CAR>
A;Residues: 1-912 < CAR>
A;Carsa-references: UNIPROT:Q78241; EMBL:Z11530; NID:g60192; PIDN:CAA77622.1; PIC;Superfamily: pol polyprotein
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CCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCCAA
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eSerLeuGluAsnThrThrAsnGlnGlnAlaGluLeuLysAlaLeuLeuLeuLeuAlaLeuGl
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Conservative:
Mismatches:
Indels:
Gaps:
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	Db 381 ValTyrTyrAspEroSe Qy 1675 TGGACCTACCAGATCTA	1735 ATGCGCACCGC 421 MetArgGlyAl	1795	1855	1915	501	521	2095 541 541	561	581	•	Oy 2335 CGCAAGGTGCTGTTCCT 	RESOLT 11 TO1668 pol polyprotein - human immunod Cispecies: human immunodeficien	C; Accession: T01668 R; Alizon, M.; Wain-Hobson, S.; (Cell 46, 63-74, 1986	A; Reference number: Z14389; MUI A; Accession: T01668 A; Status: translated from GB/EM	A; Residues: 1-902 ALL: A; Residues: 1-902 ALL: A; Cross-references: EMBL:K03456 C; Superfamily: pol polyprotein	Alignment Scores:
481 ATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAG 540 ::: :::	21 VallysGlnTyrAspGlnIlell	41 LeuvalGlykroinkrrovalAshileileGlyArgashLeuleulnkGunduguycys 80 661 ACCCTGAACTTCCCCATCAGCCCCATCAGACCGTGCCCGTGAAGCTGAAGCCCGGCATG 720	721 GACGGCCCGAAGGTGAAGCAGTGGCCCTGACCGAGGAGATCAAGGCCCTGACCGCC 780 	781 ATCTGCGAGGAGATGGAGAAGGGCAAGATCACCAAGATCGGCCCGAGAACCCCTAC 840 	841 AACACCCCGTGTTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGAC 900 	901 TTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGCAGGTGCAGCTGGGGCATCCCCCAC 960 	961 CCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACCCTACTTC 1020 	1021 AGCGTGCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCGGCATCAAC 1080 	1081 AACGAGACCCCCGGCATCCGCTACCAGTACAACGCGCTGCCCCCAGGGCTGGAAGGCAGC 1140 	1141 CCCAGCATCTTCCAGAGCAGGATGACCAGGACCCTTCCGCGCCCGCACCCC 1200	1201 GAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGC 1254	1255 CAGCACCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACC 1314 	1315 CCCGACAAGAAGCACCAGAAGGACCCCCTTCCTGGATGGGCTACGAGCTGCACCC 1374 	1375 GACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAGAGA	1435 ATCCAGAAGCTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTG 1494 	1495 CGCCAGCTGTGCAAGCTGCGCGGGGCCAAGGCCCTGACCGACATCGTGCCCCTGACC 1554 	1555 GAGGAGGCGAGCTGGAGCTGGCGGAGAACCGCGAGATCCTGCGGGGAGCCCGTGCACGGC 1614
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                                   GCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAG 1674
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TGGACGCATCGAT 2364
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deficiency virus type 1 ncy virus type 1, HIV-1 revision 20-Sep-1999 #text_change 21-Jul-2000

Gluckman, J.C.; Sonigo, P.

f. the AIDS virus: Nucleotide sequence analysis of two isol ID:86245056; PMID:2424612

MBL/DDBJ

6; NID:g60228; PIDN:CAA28012.1; PID:g60230

1465 GCOMOGNABATCTACCCOGACTOANGATGCACCACTOANGATCATCACACTOTTCACCACTOCACCACACACTOANGATCACCACACACACACACACACACACACACACACACACA	9-Jul-2004 ncy virus t
RESULTATION OF SOLVE	SOUGE SOUGH A CAN
Pred. No. 3.056-136 Length 902	Db 261 GluHisLeulLuyeTrpGlyPheThrThrProAppLysLysHisGluLysGluProPro 280 Qy 1345 TTCCTGTGGATGGGCTACGACCCCCACAAGTGGACCGTGCAGCCCATGAGCTG 1404 Db 281 PheLeuTrpMetGlyTyrGluLeuHisProAspLysTrpThrValGlnProIleGlnLeu 300 Qy 1405 CCCGAGAAGGAGGTGGACCGTGAACGACATCCAGAAGCTGGTGGCAACTGAACTGG 1464 Db 301 ProAspLysGluSerTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrp 320

unodeficiency virus type 1 in the

not compared with conceptual tran

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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Datession: A47175
R;Mohri, H.; Singh, M.K.; Ching, W.T.; Ho, D.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 25-29, 1993
A;Fitle: Quantitation of zidovudine-resistant human immunodeficiency virus type 1 in the Afforeseion: A47175; MUID:93126353; PMID:7678340
A;Accession: A47175
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual the A;Molecule type: nucleic acid
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A,CTOSH-references: UNIPROT: Q9PXX2
A)CTOSH-references: UNIPROT: G9PXX2
A)NOTE: Sequence extracted from NCBI backbone (NCBIP:122100)
C;Superfamily: pol polyprotein
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                    backbone (NCBIP:122099)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                              (1-559)
A, Residues: 1-559 <MOH>
A, Cross-references: UNIPROT: Q9PXX1
A, Note: sequence extracted from NCBI
C, Superfamily: pol polyprotein
                                                                                                                             US-09-610-313B-31 (1-2463) x B47175
                                                        2.69e-121
2771.00
96.06%
91.95%
60.59%
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Percent Similarity:
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Score: 2350.00 Matches: 440 Percent Similarity: 74.07\$ Conservative: 120 Best Local Similarity: 58.20\$ Mismatches: 152 Query Match: 51.39\$ Indels: 44 DB: 2 Gaps: 7 US-09-610-313B-31 (1-2463) x \$46347 (1-1039)	Qy 220 TTCTTCCGCGAGGACCTGCCCCAGGGCAAGGCCCGCGAGTTCCCCAGC 273	Qy 274 GAGCAGAACCGCGCCAACAGCCCCACCAGCGCGAGCTGCAGCGCGGC 324 ::: ::::	Qy 325 GACAACCCCGGAGGGCC	6	358CAGGGCACCCTGAACTTCCCCCAGATCACTGTGGCAGCCCCCCCC	403 CTGGTGAGCATCAAGGTGGGGGCGGAGTCAAGGAGGCCCTGGTGGAGACCGGGGGCGAC 1::::::::::::::::::::::::::::::::::::	Qy 463 GACACCGTGCTGGAGGAGATGAGCCTGCCGGCAAGTGGAAGCCCAAGATGGCGGGG 522	523 ATCGGCGGTTCATCAAGGTCGCCAGTACGACCAGATCTGATCGGCGCAGG	583 AAGGCCATCGGCACCGTGATCGGCCCCACCCCCGTGAACATCATCGCCGCAACATG	Qy 643 CTGACCCAGCTGGACCCTGAACTTCCCCATCAGCCCCATGGACCGTG 702	Qy 703 AAGCTGAAGCCCGGCATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGGAGAAG 762	Qy 763 ATCAAGGCCTGACCGCCATCTGCGAGGAGGAGGAGGGGGAAGGATCACCAAGATC 822		883 TGGGGAAGCTGGAGTGTGAGAGAGAGCGACCAGAGTTGGGAGGGA	Qy 943 CAGCTGGGCATCCCCGCCGCCGCCTGAAGAAGAAGAGGCGTGACCGTGCTGGAC 1002		

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CAAGATGCGCACCCCCACCACCACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGAT 1790
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
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MEDLINE=99214383; PubMed=10196340;
MOVITERY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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-!- SINITARITY: Belongs to peptidase family A2.
BEL; AFI10975; AAD17135.1;
HSSP; P04585; 1JIA.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                       540 AspGlnIleLeuIleGluIleCysGlyLysLysAlaIleGlyThrValLeuIleGlyPro
                                                                                                                                                                                                              GTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAG
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InterPro; IRROU017; integrase_C.

InterPro; IRRO0197; integrase_C.

InterPro; IRRO01995; Pepti Aspartic.

InterPro; IRRO01995; Pepti Aspartic.

InterPro; IRRO01999; Retrovir_marrix.

InterPro; IRRO01991; Retrovir_marrix.

InterPro; IRRO01911; Retrovir_marrix.

InterPro; IRRO01919; Retrov_capsid_N.

InterPro; IRRO01919; IRROSITE; PS00191; ASP_EROT_RETROV; I.

IRROSITE; PS00191; ASP_EROT_RETROV; I.

IRROSITE; PS00191; IRROCPARE; CORE; IRROSITE; PS001919; IRROSITE; PROSITE; P
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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4140.00
99.49%
99.36%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTC 72
                   Essex M.; "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from
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Protease, RNA-directed DNA polymerase, Transferase, Zinc,
                                                                                                                                                                                                    Massi, Fursos; Jour.

GO; GO:0019012; C:virion; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0008233; F:DAN binding; IEA.

GO; GO:0004523; F:RNA binding; IEA.

GO; GO:0004523; F:RNA binding; IEA.

GO; GO:0005964; F:RNA binding; IEA.

GO; GO:0005964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0005964; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:0005964; F:Rnaferase activity; IEA.

GO; GO:0005109; F:ransferase activity; IEA.

GO; GO:0006510; F:ransferase activity; IEA.

GO:0006510; F:ransferase activity; IEA.
  Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                         Botswana.";
J. Virol. 73:4427-4432(1999).
-!- SINILARITY: Belongs to peptidase family A2.
EMBL; AF110974; AAD17126.1; -.
HSSP; P04585; JJIA.
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Pfam, PF066115; RVT connect; 1.
Pfam, PF066117; RVT connect; 1.
PRNINTS; PR00399; C2HCZNRINGER.
SMARY; SM00343; ZnF CZHC; 2.
PROSITE; PS00114; ASP PROTEASE; 1.
PROSITE; PS50115; ASP—PROT RETROV; 1.
PROSITE; PS501159; ASP—PROT RETROV; 1.
AIDS; Aspartyl protease; Core protein; 1.
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Retrov capsid_C.
Retrov_capsid_N.
RNaseH.
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InterPro; IPR001969; Pept Asp AS.
InterPro; IPR010999; Retrovir_matrix.
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InterPro; IPR001031; Integrase C.
InterPro; IPR003308; Integrase Zn. V.
InterPro; IPR001995; Peptidase Zn. V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro; IPR010659; RVT connect.
interPro; IPR010661; RVT thumb.
interPro; IPR001878; Znf CCHC.
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Pfam; PF02022; Integrase;
Pfam; PF00075; RnaseH; 1.
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IPR000477; RVT
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                                                                                                                                         CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGGACCTACCAG 1686
                                                                                                                                                                                                                                       ATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCC 1746
                                                                                                                                                                                                                                                                                                                                    CACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATC 1806
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                                                                     920 IleTyrGlnGluProPheLysAsnLeuLysThrGlyLysTyrAlaLysMetArgThrAla 939
                                                                                                                                                                                                                                                                                                                                                                         HisThrAsnAspValLysGlnLeuThrGluAlaValGlnLysIleAlaMetGluSerIle 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysLeuLeuArgGlyAlaLysAlaLeuThrAspIleValProLeuThrGluGluAlaGlu 879
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SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
MOVITSKY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9WF89;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein.
Human immunodeficiency virus 1.
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                         Pfam; PF00078; RVT_1: 1.
Pfam; PF00078; RVT_connect; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00099; Zf-CCHC; 2.
PRINTS; PR0039; Zf-CCHC; 2.
PRINTS; PR0034; ZHCZNRINGER.
PRINTS; PR00141; ASP PROTRETROV; 1.
PROSITE; PS00141; ASP PROTRETROV; 1.
PROSITE; PS0175; ASP PROT RETROV; 1.
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Matches:
Conservative:
Mismatches:
Indels:
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99.49%
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Best Local Similarity:
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                                     GGCATCGGCGCAACGAGCAGATCGACAAGCTGGTGAGCCAAGGGCCATCCGCAAGGTGCTG 2346
                                                                                                                     SECUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Noviesky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
"Molecular cloning and phylogenetic analysis of human immunodeficiency
virus type I subtype C: a set of 23 full-length clones from
                     1. Virol. 779e 1 Succype C: a set of 23 full-length clones from Virol. 71:442-4432(1999).

1. Virol. 73:442-4432(1999).

1. Virol. 73:442-4432(1999).

1. SIMILARITY: Belongs to peptidase family A2.

EMBL, AD10713, AD1719.1. .

1. SIMILARITY: Belongs to peptidase family A2.

EMBL, AD10713, AD1719.1. .

1. Similarity: Belongs to peptidase activity; IEA.

GO; GO:0001901; F:aspartic-type endopeptidase activity; IEA.

GO; GO:000807; F:integrase activity; IEA.

GO; GO:000807; F:integrase activity; IEA.

GO; GO:000807; F:RNA-directed DNA polymerase activity;

R GO; GO:000873; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000870; F:transferase activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005199; F:structural molecule activity; IEA.

GO; GO:0005199; F:structural molecule activity; IEA.

InterPro; IPR00199; Retrovir_pl7.

Int
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
dag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                      PRT; 1428 AA
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                                            960 ValileTrpGlyLysThrProLysPheArgLeuProlleGlnLysGluThrTrpGluThr
                                                                                                      TGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGGAGTTCGTGAACACCCCC
                                                                                                                           CCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCCGAGACCTTC
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J. Virol. 73:4427-4432(1999).

E. SIMILARITY: Belongs to peptidase family A2.

**EMBL, API10901, AAD17021.1; -.

**RESP, Q70622; 1HVM.

**GO; GO:0019012; C:virion; IEA.

**GO; GO:0001901; F:integrase activity; IEA.

**GO; GO:0008307; F:integrase activity; IEA.

**GO; GO:000833; F:peptidase activity; IEA.

**GO; GO:0004523; F:ribonuclease H activity; IEA.

**GO; GO:0003723; F:ribonuclease H activity; IEA.

**GO; GO:0003723; F:RNA binding; IEA.

**GO; GO:0003724; F:RNA binding; IEA.

**GO; GO:0003964; F:RNA dinding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. McLane M.F., Renjifo B., Vannberg Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
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Last sequence update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroid viruses; Notures.
NCBI_TaxID=11676;
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                                            GTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAG
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       LysalaargGluPheProSerGluGlnThrargAlaIleSerProThrSerArgGluLeu
                                                      GInValArgGlyAspAsnProArgSerGluAlaGlyAlaGluGlyGlnGlyAlaLeuAsn
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PRINTS; PR00334; C2HCNFINGER.
PRINTS; PR00344; HIVIMATRIX.
SNART; SN00343; ZnF C2HC; 2.
PROSITE; PS00174; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROTEASE; 1.
PROSITE; PS50158; ZF CCHC; 2.
ZnC Finger.
Zinc-finger.
SRQUENCE 1427 AA; 160992 MW; AC2ACBF190C77DAD CRC64;
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GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0015070; F:zinc ion binding; IEA.
GO; GO:0015071; P:DNA integration; IEA.
GO; GO:0006510; P:DNA integration; IEA.
GO; GO:0006510; P:DNA recombination; IEA.
GO; GO:0006520; P:PDT-COLO951s and peptidolysis; IEA.
GO; GO:0006520; P:PDT-COLO951s and peptidolysis; IEA.
GO; GO:0016032; P:Viral life cycle; IEA.
InterPro; IPR001032; P:Viral life cycle; IEA.
InterPro; IPR001039; Integrase_Zn.
InterPro; IPR001039; Integrase_Zn.
InterPro; IPR001999; Retrovir_matrix.
InterPro; IPR001989; Retrovir_matrix.
InterPro; IPR001989; Retrovir_matrix.
InterPro; IPR001989; Retrovir_matrix.
InterPro; IPR001899; Retrovir_matrix.
InterPro; IPR001899; Retrovir_matrix.
InterPro; IPR001879; Znf_CCHC.
InterPro; IPR001979; RVT_thumb.
InterPro; IPR001979; Znf_CCHC.
IPEan; PF00077; RVP; I.
InterPro; IPR001979; Znf_CCHC.
IPEan; PF00077; RVP; I.
InterPro; IPR001979; RVT_thumb.
InterPro; IPR001979; RVT_thumb; I.
IPEan; PF000197; RVT_Thumb; I.
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R GO; GO:0019012; C:virion; IEA.

GO; GO:001419; P:aspartic-type endopeptidase activity; IEA.

GO; GO:000897; F:integrase activity; IEA.

GO; GO:000897; F:integrase activity; IEA.

GO; GO:000823; F:peptidase activity; IEA.

GO; GO:000323; F:peptidase activity; IEA.

GO; GO:000323; F:RNA binding; IEA.

R GO; GO:000396; F:RNA directed DNA polymerase activity; IEA.

R GO; GO:000396; F:RNA directed DNA polymerase activity; IEA.

R GO; GO:001674; F:RNA directed DNA polymerase activity; IEA.

R GO; GO:001674; F:RNA directed DNA polymerase activity; IEA.

R GO; GO:001674; F:RNA directed DNA polymerase activity; IEA.

R GO; GO:001674; F:RNA dependent DNA replication; IEA.

R GO; GO:0006210; F:Zinc ion binding; IEA.

R GO; GO:0006210; P:DNA recombination; IEA.

R GO; GO:0006218; P:Varaal life cycle; IEA.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol fusion polyprotein (Fragment).
                                                                                                                                                                  Viruses, Retroid viruses, Retroviridae, Lentivirus, NCBI_TaxID=11676,
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ d
-!- SIMILARITY: Belongs to peptidase family A2.
EMBL; AY255825; AAP76538.1; -.
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InterPro; IPR0001037; Integrase C.
InterPro; IPR001308; Integrase C.
InterPro; IPR001995; Peptidase_An.
InterPro; IPR001969; Pept Aspartic.
InterPro; IPR001969; Pept Aspartic.
InterPro; IPR010999; Retrovir matrix.
InterPro; IPR000071; Retrovir matrix.
InterPro; IPR008916; Retrovir p17.
InterPro; IPR008916; Retrovir p17.
InterPro; IPR008916; Retrovir p17.
InterPro; IPR008916; Retrovir p37.
InterPro; IPR008916; Retrov capsid_N.
InterPro; IPR008166; RaseH.
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InterPro; IPR010659; WT connect
InterPro; IPR010661; RVT_thumb.
InterPro; IPR001878; Znf_CCHC.
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Pfam; PF00077; RVP; 1.
Pfam; PF000778; RVP; 1.1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06811; RVT_thumb; 1.
Pfam; PF00998; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNPINGER.
                                                                                                                                            Human immunodeficiency virus 1.
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Pfam; PF00607; Gag p24; I
Pfam; PF02022; Integrase Pfam; PF00075; RnaseH; I.
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Harris M.E., Birx D.L.;
Submitted (MAR-2003) to
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    SWART; SM00343; ZNF CZHC; Z.
PROSITE; PSO141; ASP PROTEASE; 1.
PROSITE; PSO1015; ASP PROT RETROV; 1.
PROSITE; PSS0158; ZF CCHC; ZF CCHC; ALDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
NON_TER
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SEQUENCE 1429 AA; 161586 MW;
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87.10%
PR00234; HIVIMATRIX
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>	1255	CAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCGCTGGGGCTTCACCACC 1314
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	1555	GAGGAGGCCGAGCTGGAGCTGGAGAACCGCGAGATCTGCGCGAGCCCGTGCACGTGCACGTGCACGCCCGAGCTACAACGCCAAGCTGGAGAACCGCGAGAACCTGCAAGAACCTAGAAACCTAGAAACCTAAGAAACCTAAGAAACCTAAGAAACCTAAGAAACTAAAAACTAAAAAACAAAAACTAAAAAAAA
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Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
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30; GO:0008233; F:peptidase activity; IEA.
30; GO:0004523; F:ribonuclease H activity; IEA.
30; GO:0003723; F:RNA binding; IEA.
30; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.
30; GO:0005198; F:ransferase activity; IEA.
30; GO:001540; F:ransferase activity; IEA.
30; GO:001570; F:ransferase activity; IEA.
30; GO:0015074; P:DNA integration; IEA.
30; GO:0006210; P:DNA combination; IEA.
30; GO:0006218; P:RNA-dependent DNA replication; IEA.
30; GO:0006278; P:RNA-dependent DNA replication; IEA.
30; GO:0016032; P:VITAL life cycle; IEA.
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SEQÜENCE 1425 AA; 161115 MW; 782315D4D5305E18 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000721; Gag D24.
InterPro; IPR001037; Integrase C.
InterPro; IPR001037; Integrase C.
InterPro; IPR001095; Peptidase A2.
InterPro; IPR001969; Peptidase A3.
InterPro; IPR001969; Pept Aspartic.
InterPro; IPR010999; Retrovir matrix.
InterPro; IPR010999; Retrovir matrix.
InterPro; IPR008016; Retrovir p17.
InterPro; IPR008916; Retrovic p17.
InterPro; IPR008916; Retrovic gasid C.
InterPro; IPR008916; Retrovic gasid C.
InterPro; IPR008916; Retrovic gasid C.
InterPro; IPR0081165; RNaseH.
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PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02022; Integrase_Zn; 1. Pfam; PF00075; RnaseH; 1. Pfam; PF00065; rve; 1. Pfam; PF00077; RVP; 1. Pfam; PF06015; RVT_1; 1. Pfam; PF06815; RVT_consect; 1. Pfam; PF06815; RVT_chumb; 1. Pfam; PF00098; zf-CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000477; RVTse.
InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT thumb.
InterPro; IPR001878; Znf_CCHC.
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PRINTS; PR00234; HIV1MATRIX.
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97.20%
93.38%
86.49%
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Pfam; PF00607; Gag_D24; 1.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                 1018 ValGluThrPheTyrValAspGlyAlaAlaAsnArgGluThrLysIleGlyLysAlaGly 1037
                                                                                                                                                                                                                                                                                                                                                                                                                          1058 ThrGluLeuGlnAlaIleGlnLeuAlaLeuGlnAspSerGlySerGluValAsnIleVal 1077
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PubMad=14709249; DOI=10.1089/088922203771881220;
PubMad=14709249; DOI=10.1089/088922203771881220;
McCutchan F.E.;
McCutchan F.E.;
A cluster of HIV type 1 subtype C sequences from Ethiopia, observed in full genome analysis, is not sustained in subgenomic regions.";
AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family A2.
EMBL; AY258624; AAP76529.1; -.
HSSP; Q72498; 1K6Y.
GO; GO:0019012; C:virion; IEA.
GO; GO:0004190; F:sapartic-type endopeptidase activity; IEA.
GO; GO:0003677; F:iDA binding; IEA.
GO; GO:0008077; F:iDA binding; IEA.
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Kim B., McCutchan F.E.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol Lusion polyprotein (Fragment).
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SEQUENCE FROM N.A.
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                                                                                                                                                                            "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                                                                                        [1] — SEQUENCE FROM N.A. SEQUENCE FROM N.A. Noblem M.P., Renjifo B., Vannberg F., Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Warlink R., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Foley B.T., ndung'u T.P., Rahman M., Makhema M.J., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Foley B.T., Ndung'u T.P., Rahman immunodefici
                                                                                                                                                                                                                University (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
63-pol polyprotein:
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                             1427 AA
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Interpro; IPR0010370; Integrase_C.
Interpro; IPR0010370; Integrase_C.
Interpro; IPR0010370; Integrase_C.
Interpro; IPR001995; Peptidase_ZZ.
Interpro; IPR001995; Peptidase_ZZ.
Interpro; IPR001999; Retrovir_matrix.
Interpro; IPR0010999; Retrovir_matrix.
Interpro; IPR0010991; Retrovir_matrix.
Interpro; IPR0010991; Retrovir_p107.
Interpro; IPR001184; Retrov_capsid_C.
Interpro; IPR001184; RVe.
Interpro; IPR001184; RVe.
Interpro; IPR011669; RVT_connect.
Interpro; IPR0106691; RVT_connect.
Interpro; IPR0106691; RVT_connect.
Interpro; IPR010661; RVT_thumb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fram, Pro00099; Z-CCHC; Z-CCHC; Pfam, PRO00099; Z-CCHC; Z-CCHCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
SWART; SM00343; ZnF CZHC; Z.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROTEASE; 1.
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Pfam; PF00660; Gag_D24; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; RasseH; 1.
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Pfam; PF06815; RVT connect; 1.
Pfam; PF06817; RVT thumb; 1.
                             PRELIMINARY;
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PF00077; RVP; 1
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Pfam;
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AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc; Zinc-finger. Sinc-finger 1427 AA; 160518 MW; FBDA73D603A68B18 CRC64;
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3948.00
97.07%
92.88%
86.33%
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Percent Similarity:
Best Local Similarity:
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the EMBL/GenBank/DDBJ
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SEQUENCE FROM N.A.
Harris M.E., Birx D.L.;
Submitted (MAR-2003) to
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Kim B., McCutchan F.E.;
Submitted (MAR-2003) to
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PheAlaIleLysLysAspSerThrLysTrpArgLysLeuValAspPheArgGluLeu
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AlaIleGlnLeuAlaLeuGlnAgpSerGlyAlaGluValAsnIleValThrAspSerGln
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GO:0004190; F:aspartic-type endopeptidase activity; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0008937; F:integrase activity; IEA.
GO:0008233; F:peptidase activity; IEA.
GO:0004523; F:ribonuclease H activity; IEA.
GO:0003723; F:RNA binding; IEA.
GO:0003964; F:RNA directed DNA polymerase activity; IEA.
GO:0005198; F:structural molecule activity; IEA.
GO:0006740; F:structural molecule activity; IEA.
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GEX4R4;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annocation update)
GS-JUL-2004 (TrEMBLrel. 27, Last annocation update)
GAG-Pol fusion polyprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Manyan S., Zelra M. A.

Manyan S., Zelra M. A.

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ data
-1- SIMILARITY: Belongs to peptidase family A2.

EMBL; AY255823, AAP76521.1; -

EMBL; AY255823, AAP76521.1; -

EMBL; AY255823, AAP76521.1; -

GO; GO:00019012; C:virion; IEA.

GO; GO:00019012; C:virion; IEA.

GO; GO:00003677; F:DA binding; IEA.

GO; GO:0008233; F:DA binding; IEA.

GO; GO:0008233; F:Peptidase activity; IEA.

GO; GO:0003523; F:RA binding; IEA.

R GO; GO:000354; F:RAA binding; IEA.

R GO; GO:0003564; F:RAA binding; IEA.

R GO; GO:0003564; F:RAA binding; IEA.

R GO; GO:0003564; F:RAA directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:RAA directed DNA polymerase activity; IEA.
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GO; GO:0008270; F:zinc ion binding; IEA.

GO; GO:0005301; P:DNA integration; IEA.

GO; GO:0006230; P:DNA integration; IEA.

GO; GO:0006230; P:DNA integrated:

Red; GO:0006230; P:VIXE1 lite cycle; IEA.

GO; GO:0006230; P:VIXE1 lite cycle; IEA.

RICETPO: IPRO0137; Integrase C.

BR InterPo: IPRO0137; Integrase C.

BR InterPo: IPRO0137; Integrase C.

RICETPO: IPRO0139; Pept Maparitic.

BR InterPo: IPRO0199; Pept Maparitic.

BR InterPo: IPRO0199; Retrovir pl.

RICETPO: IPRO0199; Retrovir pl.

REAM: PRO0199; RVT 1.

REAM: RRINTS; RRO0199; RVT 1.

REAM: RRINTS; R
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SEQÜENCE 1430 AA; 161540 MW; 5BBA39B85D03FA0B CRC64;
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Matches:
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                             CGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACC 1554
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                                                                        GluGluAlaGluLeuGluLeuAlaGluAsnArgGluIleLeuLysGluProValHisGly 898
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
J. Virol. 73:4427-4432(1999).
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Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
MOVIESKY V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
                                                                                                                                                                                                                                                                                                                              R GO; GO:0019012; C:virion; IEA.

R GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

R GO; GO:0008907; F:nDNA binding; IEA.

R GO; GO:0008233; F:DNA binding; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0003723; F:ribonuclease H activity; IEA.

R GO; GO:0003723; F:RNA binding; IEA.

R GO; GO:0005198; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:Rructural molecule activity; IEA.

R GO; GO:0005198; F:rincion binding; IEA.

R GO; GO:0005070; F:rincion binding; IEA.

R GO; GO:000508; F:princion binding; IEA.

R GO; GO:0006218; F:RNA-directed DNA recombination; IEA.

R GO; GO:0006218; P:PNNA-dependent DNA replication; IEA.

R GO; GO:0006218; P:Princion binding; IEA.
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                                 Gag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to peptidase family A2 EMBL; AF110964; AAD17047.1; -.
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Pept_Asp_AS.
Retrovir_matrix.
Retrovir_pl7.
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PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZF_CCHC; 2.
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InterPro, IPR001037; Integrase_C.
InterPro, IPR001308; Integrase_Zn_N.
InterPro, IPR001995; Peptidase_A2_
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InterPro; IPR010661; RVT_thumb.
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PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
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Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00098; zf-CCHC; 2.
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Integrase_2
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IPR000477; RVTE
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PF00077; RVP; 1
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Alignment Scores:

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PRT; 1427

01-NOV-1999 (TrEMBLrel. 12, Created)

Q9WF71; Q9WF71

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PRELIMINARY;

Pred. No.: 4.96e-148 Length: 1427 Score: 3935.50 Matches: 727 Percent Similarity: 96.95\$ Conservative: 35 Best Local Similarity: 92.49\$ Mismatches: 21 Onery Match: 3 1742 1742	& & &	973 AAGAAGAAGAAGAGCGTGACCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTG 1032
2 Gaps: 2 Gaps: 13E-21 (1-2462) & COMP71 (1-1427)	d G	0 AspGluSerPheArgLysTyrThrAlaPheThrIleProSerIleAsnAsnSerThrPro 71
CCGAGGCCATGAGCCAGG	Qy Dp	3 GGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTC 1
AAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGCCATCGCCCCGC	oy G	3 CAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATC
AGATG 1 	රු සි	7
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AAGGCCGCGAGTTCCCCAGCGAGCAGCACCGCCCCACAAGCCCCCACCGCGAGCTG 31 :::	λ Q	1327 CACCAGAAGGAGCCCCCTTCCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACC 1386
CAGGTGCGCGACAACCCCGCAGCGAGGCGCGCCGAGCGCCAGGCACCCTGAAC 3	ζς G	1387 GTGCAGCCCATCGAGCTGCCCGAGAGCAGAGCTGGACCGGAACGACATCCAGAAGCTG 1446
TTCCCCCAGATCACCTGTGGCAGCCCCCTGGTGACACATCAGGTGGGCGCCGCAGATC 43 TTCCCCCCAGATCACCCTGTGGCAGCCCCCCTGGTGAGCATCAAGGTGGGCGCGCAGATC 43 TTCCCCCAGATCACTGTGGCAGCCCCCCTGGTGAGCATCAAGGTGGGCGCGCAGATC 43 TTCCCCCAGATCACTGTTACTTACTTACTATACTATACT	ò a	1447 GTGGGCAAGCTGAACTGGGCCAGCCAGCCAGCCTCAGCCTCAAGGTGCGCCAGCTGTGC 1506 :::
AAGGAGGCCCTGCTGGACACCGGCGACGACGACGTGCTTGCT	S da	1507 AAGCTGCTGCGGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGCCGAG 1566
GGCAAGTGGAAGCCCAAGATGATCGCGGCCATCGCGGCTTCATCAAGGTGCGCCAGTAC 55	ζς G	1567 CTGGAGCTGGCGAGAATCCTGCGCGAGCCCGTGCACGCGTGTACTACGAC 1626
GACCAGATCCTGATCGGGGAAGAGGCCATCGGCACCGGGCTGATCGGCCCC 61 :::	S d	1627 CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAG 1686
ACCCCCGTGAACATCATCGGCCGCAACATGCTGACCAGCTGGCTG	S G	1687 ATCTACCAGGAGCCCTTCAAGAACCTCAAGACCGGCAAGTACGCCAAGATGCGCACCGCC 1746
SOLATE 57 CCAAG 73 [Cy GD	1747 CACACCAACGAGGGGAGCTGACCGAGGCCGTGCAAGATCGCCATGGAGGCCTC 1806
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MetGluLysGluGlyLysllefintLyslleGlyProGluAsnProlyrasnintFroval 63 TTCGCCATCAAGAAGAAGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTG 91	y da	1927 CCCCTGGTGAAGCTGTGGTACCAGCTGGAAGAAGAGCCCATCATCGGCGCCGAGACCTTC 1986
640 PheAlaileLysLysSperintLysTipArglysLeuvalAspPheArgGlubeu 659 913 AACAAGGGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGCCGCCGCCTG 972	S S	1987 TACGTGGACGGCCCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGAC 2046
660 AsniysArgThrdinAspPheTrpGluValdinLeuGlyileProHisProAlaGlyLeu 679	۵ ا	7 CGGGGCCGGCAGAAGATCGTGAGCTGACCGAGACCACCAGCAGAAGACCGAGGTGCAG 210

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Pfam; PF00540; Gag pl7
Pfam; PF00607; Gag p24
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Best Local Similarity:
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DB:
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MEDLINE=99214383; PubMed=10196340;
MEDLINE=99214383; PubMed=10196340;
Movitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Mdung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
Essex M
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GO; GO:0019191; C:virion; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:000317; F:DNA binding; IEA.

GO; GO:0008233; F:petidase activity; IEA.

GO; GO:0008233; F:petidase activity; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:000570; F:transferase activity; IEA.

GO; GO:0005818; P:NNA-dependent DNA replication; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

GO; GO:0006508; P:viral life cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
6ag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR001037; Integrase C.
InterPro; IPR0010308; Integrase Zn. N.
InterPro; IPR001995; Peptidase A2.
InterPro; IPR001995; Peptidase A2.
InterPro; IPR001969; Pepti Aspartic.
InterPro; IPR001999; Retrovir_matrix.
InterPro; IPR000071; Retrovir_matrix.
InterPro; IPR000071; Retrovir_matrix.
InterPro; IPR0009916; Retrovir_matrix.
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                                                                                                                                                                                                                                                                                                                                                                                                          AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
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Matches:
Conservative:
Mismatches:
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PRINTS; PRO0234; HIVIMATRIX.
SWART; SM00343; ZnF C2HC; 2.
PROSITE; PSO0141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROY; 1.
PROSITE; PS50175; ASP CCHC; 2.
AIDS; ABDAXTY] protease; Core protein;
Retrov_capsid_N. RNaseH.
                                        InterPro; IPR010659; RVT connect.
InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT thumb.
>fam; PF0ner.
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Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; RnaseH; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00077; RVP; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
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CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAG 1686
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             GTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGCACCTGGGAGACC
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                                                       ATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAAGATGCGCACCGCC
                                                                      CACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGGAGCATC
                                                                                                                                Gag-pol polyprotein.

Human immunodeficiency virus 1.

Human immunodeficiency virus 1.

NCBI TaxID=11676;

(1)

SEQUENCE FROM N.A.

MEDLINE=99214383; PubMed=10196340;

NoviteKy V.A., Montano M.A., McLane M.F., Renjifo B., Vannber Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R. Essex M.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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virus type 1 subtype C: a set of 23
Botswana.";
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                                                 AAGGCCCGCGAGTTCCCCCAGCGAGCAGAACCGCCCCAACAGCCCCCACCAGCCGCGAGCTG
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AIDS; Aspartyl protease; Core protein; Hydrolase; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase. SEQUENCE 1427 AA; 161347 MW; 595F19865DE81D63 CRC64;
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Pfam; PP00607; Gag_D24; I.
Pfam; PP00607; Gag_D24; I.
Pfam; PP006075; RnaeH; I.
Pfam; PP00075; RvP; I.
Pfam; PP00077; RvP; I.
Pfam; PP008078; RVP; I.
Pfam; PP00815; RVP; Connect; I.
Pfam; PP06815; RVT; Connect; I.
Pfam; PP06815; RVT; Connect; I.
Pfam; PP06815; RVT; Connect; I.
Pfam; PP00814; RVT; Chumb; I.
Pfam; PP00814; ZnF CCHC; 2.
SMART; SN00343; ZnF CCHC; 2.
PROSITE; PS50175; ASP PROTEASE; I.
PROSITE; PS50175; ASP PROTEASE; I.
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Best Local Similarity:
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"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BOLLINE-29214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        History, 274736; INCP.

RGO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

RO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

RO; GO:0003967; F:DNA binding; IEA.

RO; GO:000423; F:peptidase activity; IEA.

RO; GO:000423; F:peptidase activity; IEA.

RO; GO:000423; F:peptidase activity; IEA.

RO; GO:000423; F:rhonnclease H activity; IEA.

RO; GO:000423; F:RNA-directed DNA polymerase activity; IEA.

RO; GO:000519; F:RNA-directed DNA polymerase activity; IEA.

RO; GO:000519; F:RNA-directed DNA polymerase activity; IEA.

RO; GO:000510; F:ransferase activity; IEA.

RITHERPO; IPRO01999; Retrovir_matrix.

RITHERPO; IPRO01999; Retrovir_matrix.
                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 73:4427-4432(1999).
-!- SIMILARITY: Belongs to peptidase family A2.
EMBL; AF110967; AAD17072.1; -.
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InterPro; IPR010661; RVT thumb.
InterPro; IPR001878; Znf CCHC.
                              2347 TTCCTGGACGGCATCGAT 2364
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Pfam; PF00077; RVP; 1.
Pfam; PF000778; RVT 1; 1.
Pfam; PF06815; RVT connect; 1.
Pfam; PF06815; RVT chunb; 1.
Pfam; PF00098; zf.CCHU, 2.
PRINTS; PR00939; CZHCZNFINGER.
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SMART; SM00343; ZnF_C2HC; 2.
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PF02022; Integrase_Z
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                                                                                                                                                                             PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                           Gag-pol polyprotein.
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Pfam;
Pfam;
Pfam;
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PROSITE; PS50175; ASP_PROT_RETROV; 1.
PROSITE; PS50158; ZF CGHC; 2.
ALDS; Aspartyl protease; Core procein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
SEQUENCE 1437 AA; 161978 MW; 65DAA25678717176 CDC64.
                                                                                                                                                                     AACTGCCGCGCCCCCCCCAAGAGGCCTGCTGGAAGTGCGGCAAGGAGGGCCCACAGATG
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Indels:
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                                                     Alignment Scores:
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ą		sTrpGlyPheThrThrProAspLysLysHisGlnLysGluProProPheLeuTrpMet 81
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≿	1717	AAGATGCGCACCGCCCACACCAACGACGTGAAGCAGCTGACCGAG 17
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≱ . 4	1777	GCCGTGCAGAAGATCGCCATGGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGC 1836
		ATCCAGAAGGAGACCTGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGG 18
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420 LysAspCysThrGluArgGlnAlaAsnPhePheArgGluAsnLeuAlaPheProGlnGly 439
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PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZE CHC; 2.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
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Gag_p24.
Integrase_C.
Integrase_Zn_N.
Peptidase_A2.
Pept_Aspartic.
Pept_Aspartic.
Pept_Aspartic.
Retrovir_matrix.
Retrovir_matrix.
Retrov_capsid_C.
Retrov_capsid_N.
Retrov_capsid_N.
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RVT_connect.
RVT_thumb.
Znf_CCHC.
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InterPro; IPR001584; Rve.
InterPro; IPR000477; Rve.
InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT thumb.
InterPro; IPR010661; RVT thumb.
Fram; PF00540; Gag_p17; I.
Pfam; PF00607; Gag_p24; I.
Pfam; PF00602; Integrase_Zn; I.
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3919.50
96.82%
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85.71%
                                 Interpro; IPR003308; In
Interpro; IPR001995; Pe
Interpro; IPR001969; Pe
Interpro; IPR010999; Re
Interpro; IPR010999; Re
Interpro; IPR008916; Re
Interpro; IPR008916; Re
                     PR001037;
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                     AGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGCCC
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                                                                             AAGGAGCCCATCATCGGCGCCCGAGACCTTCTACGTGGACGGCCCCCAACCGCGAGACC
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BEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GG; GG:001901; C:virion; IEA.
GG; GG:001919; F:aspartic-type endopeptidase activity; IEA.
GG; GG:000319; F:DNA binding; IEA.
GG; GG:000317; F:DNA binding; IEA.
GG; GG:0008233; F:peptidase activity; IEA.
GG; GG:0008233; F:peptidase activity; IEA.
GG; GG:0003723; F:RNA binding; IEA.
GG; GG:0003723; F:RNA-directed DNA polymerase activity; IEA.
GG; GG:0003729; F:RNA-directed DNA polymerase activity; IEA.
GG; GG:0005198; F:structural molecule activity; IEA.
GG; GG:0006519; F:zinc ion binding; IEA.
GG; GG:0006508; P:DNA integration; IEA.
GG; GG:0006508; P:DNA recombination; IEA.
GG; GG:0006508; P:Proceolysis and peptidolysis; IEA.
GG; GG:0006508; P:Proceolysis and peptidolysis; IEA.
GG; GG:0006508; P:viral life cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGCCATCGAT 2364
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 26, Last annotation update)
639-pol polyprotein.
Human immunodeficiency virus 1.
Viruses, Retroid viruses; Retroitidae, Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 73:4427-4432(1999).
-!- SIMILARITY: Belongs to peptidase family A2.
EMBL; AF110965; AAD17056.1; -.
PIR; S49086; S49086.
HSSP; Q70622; 1HVN.
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MEDLINE-22375625; PubMed=12487816; DOI=10.1089/088922202320886325; MEDLINE-22375625; PubMed=12487816; DOI=10.1089/088922202320886325; MEDLINE-22375625; MEDLINE-2.R., Kim B., Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T., Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L., McCutchan F.B.; McCutchan F.B.; "Among 46 near full length HIV type 1 genome sequences from Rakai District, Uganda, subtype D and AD recombinants predominate."; AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

-I- SintlarITY: Belongs to peptidase family A2.

EMBL, AF444491; AAN73556.1;

HSSP; P24736; INCP.
                                                                                                                                                                                                                                                                                                                             Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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Harris M.E., Birx D.L., Robb M.L.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR009007; Pept Aspartic.
InterPro; IPR001969; Pept Aspartic.
InterPro; IPR001969; Retrovir_matrix.
InterPro; IPR000011; Retrovir_matrix.
InterPro; IPR0008916; Retrov Capsid_C.
InterPro; IPR0008919; Retrov Capsid_N.
InterPro; IPR001566; RNaseH.
InterPro; IPR001684; RVe.
InterPro; IPR016699; RVT.
InterPro; IPR010661; RVT.
INTERPRO; RV
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GO; GO: 0003677; F: DNA binding; IEA.
GO; GO: 0008937; F: prepridase activity; I
GO; GO: 0008233; F: prepridase activity; I
GO; GO: 0008233; F: ribonuclease H activi
GO; GO: 0003737; F: RNA-binding; IEA.
GO; GO: 0003798; F: RNA-directed DNA poly
GO; GO: 000198; F: structural molecule a
GO; GO: 0001674; F: stransferase activity;
GO; GO: 0001870; F: stransferase activity;
GO; GO: 0001871; P: DNA integration; IEA.
GO; GO: 0001808; P: RNA-dependent DNA reg
GO; GO: 0001808; P: RNA-dependent DNA reg
GO; GO: 0016032; P: viral life cycle; IEA
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InterPro; IPR001308; Integrase_Zn N.
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PF06815; RVT_connect; 1.
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Pfam; PF06817; RVT_thumb; 1.

Phfam; PF00098; zf-CCHC; 2.

SMART; SM00343; ZnF CZHC; 2.

PROSITE; PS00141; ASP_PROTEASE; 1.

PROSITE; PS50175; ASP_PROT_RETROV; 1.

PROSITE; PS510158; ZF_CCHC; 2.

AIDS; Asparty1 protease; Core protein; Hydrolase; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase.
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SEQUENCE 1427 AA; 161058 MW; 20559041E2A88B5C CRC64;
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Matches:
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menson, m.;
molecular cloning and phylogenetic analysis of human immunodeficiency
NT virus type 1 subtype C: a set of 23 full-length clones from
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NT virus type 1 subtype C: a set of 23 full-length clones from
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MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.

Viruses, Retroid viruses, Retroviridae, Lentivirus.
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GO; GO:0006278; P:RNA-dependent DNA replic GO; GO:0016032; P:Yiral life cycle; IEA. InterPro; IPR001037; Gag_p24.

InterPro; IPR001037; Integrase C. InterPro; IPR001039; Integrase A2. InterPro; IPR001995; Peptidase A2. InterPro; IPR001995; Retrovir_matrix. InterPro; IPR001991; Retrovir_p17. InterPro; IPR001991; Retrovir_p17. InterPro; IPR001916; Retrovir_p17. InterPro; IPR001916; Retrovir_p17. InterPro; IPR001959; Retrovir_p17. InterPro; IPR001959; Retrovir_p17. InterPro; IPR001959; RVT connect. InterPro; IPR001959; RVT connect. InterPro; IPR001959; RVT connect. InterPro; IPR00197; RVP; I. Pfam; PF00075; RVP; I. Pfam; PF00075; RVP; I. Pfam; PF000075; RVP; I. Pfam; PF000198; RVT chumb; I. Pfam; PF000198; RVT chumb; I. Pfam; PF000198; RVT chumb; I. Pfam; PF000198; Zf-CCHC; Z. PRINTS; PR00198; Zf-CCHC; Z. RRINTS; PR00198; Zf-CCHC; Z. RRINTS; PR00198; Zf-CCHC; Z. RRINTS; PR00198; Zf-CCHC; Z. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROV; I. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROV; I. PR051TE; PS00114; ASP-PROT RETROV; I. PR051TE; PS00115; ASP-PROT RETROVICE; I. PR051TE; PS00115;
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APPLICANT: Swanstrom, Robert Edward
APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Warris, Lynn
APPLICANT: Williamson, Carolyn
TITLE OF INVENTION: Subcype Isolates, Their Genes nd Modifications and Derivatives Ti
TITLE OF INVENTION: Subcype Isolates, Their Genes nd Modifications and Derivatives Ti
FILE REPERENCE: 45669-281993
CURRENT APPLICATION NUMBER: US/10/332,413
FURR RAPPLICATION NUMBER: US 60/216,995
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: ZA 2000/3437
PRIOR PELING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: ZA 2000/4924
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-MODEL=frame+ n2p.model - DEV=xlh
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-D=Published Applications AA -QFWT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
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-TRANS=human40.cdi -L1ST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-NCPUG- CICUPAT - NAMAD -LAGREQUERY - NEG SCORES=0 - WAIT -DSPBLOCK=100
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-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 1, Appli Sequence 1, Appli Sequence 29, Arri Sequence 29, Arri

Sequence 10, Sequence 1,

Sequence 14, Al Sequence 14, Sequence 2, Al Sequence 87,

Sequence 118, App Sequence 88, Appl Sequence 3, Appli

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            AGCGACCTGGAGATCGGCCAGCACCGCCCAAGATCGAGGAGCTGCGCAAGCACCTGCTG
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    (1-2463) x US-10-332-413-4 (1-998)
                                     virus type
                                                                                         Gaps:
                              TYPE: PRT ORGANISM: Human immunodeficiency
                                                           1.56e-165
3570.00
97.07%
93.02%
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 998
                                                     Alignment Scores:
Score:
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Query Match:
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280 AACCGCGCCAACCACCACCGCGAGCTGCAGGTGCGCGCGACCAACCCCCGCAGC 339 160 ThrArgAlaAsnSerProThrSerArgGluLeuGlnValArgArgAspAsnProArgSer 179 340 GAGGCCGACGCGCAGGCACCCTGAACTTCCCCCAGATCAACCTGCAGCG 399 180 GluThrGlUArglysGlyThrLeuAsnPheProGln1leThrLeuTrpGlArg 199 400 CCCTGGTGAGCATGACGGCGCCAGATCAAGGAGCCCTGTGGCACCC 459 1	460 GACGACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGC 519 	520 GGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGC 579	260 LysLysAlalleGlyThrValLeuValGlyProThrFroValAsnIleIII	GTGAAGCTGAAGCCCCGCACGACGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAG	760 AAGATCAAGGCCCTGACCGCCATCTGCGAGGAGTAGGAGGAGGAGGGGAAGATCACCAAG 819 	820 ATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGGACAGCACC 879 	880 AAGTGGCGCAAGCTGGCGAGCTGCAACAGCGCACCCAGGACTTCTGGGAG 939 	940 GTGCAGCTGGGCATCCCCCACCCCGCCCGAAGAAGAAGAAGAAGAAGGAGCGTGACCGTGCTG 999	1000 GACGTGGCGACGCCTACTTCAGCGTGCCCTGGAGGACTTCCGCAAGTACACCGCC 1059 	1060 TTCACCATCCCCAGCATCAACAACAACCCCCGGCATCCGCTACCAGTACAACGTGCTG 1119	1120 CCCCAGGGCTGGAGGGGGGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAG 1179 	CCCTTCCGCGCCCGCAACCCCGAGATCTACCAGGCCCCCTGTACGTG	1234 GGCAGCGACCTGCAGCACCAGCACCGCGCCAGATCCAGGACTGCGCAAGGACCTG 1293 	1294 CTGCGCTGGGGCTTCACCACCCCGACAAGAACACCACAAAAGGAGCCCCCTTCCTGTGG 1353 :::
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280 AACCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTG-----CGCGGCGACAACCCC 333
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TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (IV9) COMPOUNDS
TITLE REFERENCE: 62 2112.00
CURRENT APPLICATION WINBER: US/10/283,847
CURRENT FILING DATE: 2002-10-29
RIOR APPLICATION NUMBER: 60/345,116
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 17
SSEQ ID NO 17
LENGTH: 1003
                                                                                                                                                                                                                                                 US-09-610-313B-31 (1-2463) x US-10-283-847-17 (1-1003)
                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  ORGANISM: Human Immunodeficiency Virus
APPLICANT: Nicolette, Charles A.
                                                                                                                                                                          5.48e-162
3497.00
95.56%
90.85%
76.47%
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Sequence 17, Application US/10283847 Publication No. US20030162720A1 GENERAL INFORMATION:

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Qy 1306 TTCACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGTGGATGGGCTACGAG 1365 Db 381 LeuThrThrProAspLysLysHisGlnLysGluProProProPheLeuTrpMetGlyTyrGlu 400 Qy 1366 CTGCACCCCGACAAGTGGACCCTGCACCCATCGAGCTGCCCGAGAAGCTGGACC 1425 Db 401 LeuHisProAspLysTrpThrValGlnProIleValLeuProGluLysAspSerTrpThr 420 Qy 1426 GTGAACGACTACCAGAAGCTGGCCAAGCTGACCAGCCAGATCTACCCCGGC 1485 Db 421 ValAsnAspIleGlnLysLeuValGlnPysLeuAsnTrpAlaSerGlnLieTyProGly 440 Qy 1486 ATCAAGGTGCGCGCGCGCGCCGCCCGCCCGAAGCTGACCGCAACCTGACCGAAACCTGACGAATCGTG 1545 Qy 1486 ATCAAGGTGCGCGCGCGCGCGCGCGCCGAAGCCCGAACCCGCCGTGACCGCCGCTGACCGCCGCTGACCGCCGCTGACCGCCGCTGACCGCTGACCCGCTGACCCGCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCCTGACCTGACCTGCTCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACTGTCTGT	Db 441	Qy 1666 CACGACCAGTGGACCTACCAGAGCCCTTCAAGAACCTGAAGACCGCAAG 1725	Qy 1786 AAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAGATCCGCCTGCCCCATC 1845 Db 541 LyslleThrThrGluSerIleVall1eTrpGlyLysThrProLysPheLysLeuProlle 560 Qy 1846 CAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGCCAGGTCCCCGAG 1905 Db 561 GlnLysGluThrTrpGluThrTrpTrpThrGluTyrTrpGlnAlaThrTrpIleProGlu 580	Qy 1906 TGGGAGTTCGTGAACACCCCCCCCGGTGAAGCTGTGGTAGTAGTAGTAGAAGGAGCCC 1965 Db 581 TrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGluLysGluPro 600 Qy 1966 ATCATCGGCCCGAACCTCTCTACGTGGACGCCCCCCAACCAA	Qy 2026 AAGGCCGGCTACGTACCGACCGGCCGGCAGAAGATCGTGAGCCTGACCGACACCCACC		2266 AGCTGGCCGCCCACAAGGCATCGGCGACGAGCAGAGAGAG
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| ThrArgAlaAsnSerProThrIleSerSerGluGlnThrGlyAlaAsnSerProThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: protein encoded by construct of vaccine vector; OTHER INFORMATION: pGA2 and insert JS2 expressing clade HIV-1 VL US-10-093-953A-26
                                                    GENERAL INFORMATION:
APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Hua, Jian
APPLICANT: Wass, Bernard
APPLICANT: Wast, Linda
APPLICANT: Watt, Linda
APPLICANTION: AND MERR: US 0/10/093, 953A
CURRENT APPLICATION NUMBER: US 60/251,083
PRIOR PELING DATE: 2000-03-02
PRIOR PELING DATE: 2000-12-01
PRIOR PELING DATE: 2001-03-02
PRIOR PELING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOCIENARE: FREEER FREER FREEER FREER 
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               Sequence 26, Application US/10093953A Publication No. US20040105871A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity:
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                                                                                                                                                                                                                                           OTHER INFORMATION: protein encoded by construct of vaccine vector OTHER INFORMATION: pGA1 and vaccine insert expressing clade B HIV-1 OTHER INFORMATION: Gag-Pol
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Mismatches:
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Matches:
              PRIOR APPLICATION NUMBER: PCT/USO1/06795
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FESTSEQ for Windows Version 4.0
SEQ ID NO 31
LENGTH: 739
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3452.00
93.45%
88.81%
75.49%
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ORGANISM: Artificial Sequence
FEATURE:
   FILING DATE: 2001-03-02
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Best Local Similarity:
Query Match:
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APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Hua, Jian
APPLICANT: Hua, Jian
APPLICANT: Hua, Jian
APPLICANT: Mara, Rama
APPLICANT: Myatt, Linda
APPLICANT: Barl, Patricia
TITLE OF INVENTION: AN IMMUNE RESPONSE
FILE OF INVENTION: AN IMMUNE RESPONSE
FILE OF INVENTION: AN IMMUNE RESPONSE
FILE SEPERENCE: 1204-005602
CURRENT PALICATION NUMBER: US/10/093,953A
CURRENT FILING DATE: 2002-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: US 60/251,083
PRIOR PILING DATE: US 09/798,675
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                                                     AACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTG
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US-10-325-468-23

Sequence 23, Application US/10325468

Publication No. US20040101823A1

GENERAL INFORMATION:

APPLICANT: Scong, Nay Wei

APPLICANT: Schibata, Natia

TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL

TITLE OF INVENTION: HOWELS OF HIV-1 PATHOGENESIS

FILE REPERBURE: 0166-2110US

CURRENT APPLICATION NUMBER: US/10/325,468

CURRENT FILING DATE: 2002-12-19

PRIOR RILING DATE: 2001-12-21

NUMBER OF SEC ID NOS: 56

SOFTWARE: FastSEC for Windows Version 4.0

LENGTH: 1003
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AACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGACGCACCAAGTGGCGCAAG
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GCCGCCTACCTGACCGACGGCGCAGAAG 2061 2301 GGCATCCGCAAGGTGCTGTTCCTGGACGCCATC 2361 AACCACATCCAGAAGCTGGTGGGCAAGCTGAAC 1461 GACCAGIGGACCTACCAGATCTACCAGGAGCCC 1701 ATCGCCATGCAGAGCATCGTGATCTGCGGCCAAG 1821 1941 ATCGTGACCGACAGTACGCCCTGGGCATC 2181 AGCGAGCTGGTGAACCAGATCATCGAGCAGCTG 2241 CAGAAGACCGAGCTGCAGGCCATCCAGCTGGCC 2121 CTGACCGAGGCCGAGCTGGAGCTGGCCGAG 1581 ATCGGCGCCGAGACCTTCTACGTGGACGCGCC 2001 640

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US-10-325-468-35
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APPLICANT: Soong, Nay Wei
APPLICANT: Pekrun, Katja
APPLICANT: Shibata, Riri
TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
FILE REPERENCE: 0166.210US
CURRENT APPLICATION NUMBER: US/10/325,468
CURRENT FILING DATE: 2002-12-19
PRIOR PILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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94.73$
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                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                               TrpTyrGlnLeuGluLysGluProlleValGlyAlaGluThrPheTyrValAspGlyAla
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APPLICANT: Pekrun, Katja

APPLICANT: Soong, Nay Wei

APPLICANT: Pekrun, Katja

APPLICANT: Pekrun, Katja

APPLICANT: Pekrun, Katja

TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS

FILE REFERENCE: 0166.210US

CURRENT APPLICATION NUMBER: US/10/325,468

CURRENT APPLICATION NUMBER: US 60/343,524

PRIOR APPLICATION NUMBER: US 60/343,524

PRIOR APPLICATION NUMBER: US 60/343,524

PRIOR APPLICATION NUMBER: US 60/343,524

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1003
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; Publication No. US20040101823A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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Percent Similarity:
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Pred. No.:
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US-10-325-468-20
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; Sequence 20, Application US/10325468
; Publication No. US20040101823A1
; GENERAL INFORMATION:
; APPLICANT: Soong, Nay Wei
; APPLICANT: Soong, Nay Wei
; APPLICANT: Shibata, Riit
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; CURRENT APPLICATION NUMBER: US/10/325,468
; CURRENT APPLICATION NUMBER: US/10/325,468
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/343,524
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 20
; SEQ ID NO 20
; LENGTH: 1003
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Matches:
Conservative:
Mismatches:
Indels:
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3427.00
94.59%
88.49%
74.94%
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ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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ThrGlyAlaAsnSerSerAlaSerArgLysLeu------GlyAspGly-----
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                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
   uses
; TITLE OF INVENTION: Synthetic molecules and use; FILE REFERENCE: Savine CURRENT APPLICATION NUMBER: US/10/296,734; CURRENT FILING DATE: 2003-08-04; PRIOR APPLICATION NUMBER: AU PQ7761/00; PRIOR FILING DATE: 2000-05-26; NUMBER OF SEQ ID NOS: 1507; SOFTWARE Patentin version 3.2; SEQ ID NO 1470; LENGTH: 995
                                                                                           Human immunodeficiency virus
                                                                                                                           1.61e-157
3405.00
94.17%
88.61%
74.46%
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                            ; ORGANISM: Humar
US-10-296-734-1470
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Pred. No.:
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NAME/KEY: MISC FEATURE
LOCATION: (53)...(55)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (130)..(130)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (1737..(173)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (1977..(197)
OTHER INFORMATION: X = unknown amino acid
                                                                                    LOCATION: (48)...(48)
OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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LOCATION: (194<sup>7</sup>..(194)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (255)..(255)
OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC_FEATURE
LOCATION: (293)..(293)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (300)...(300)
OTHER INFORMATION: X = unknown amino acid
FEATURE:
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LOCATION: (316)..(316)
JTHER INFORMATION: X = unknown amino acid
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LOCATION: (320)..(320)
OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (280)..(281)
OTHER INFORMATION: X = unknown amino acid
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                                          2065 GTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCTG
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                                                                  594 SerArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysVal 613
                                                                                                                                                                                                                                                                                                                        ## Sequence 1471, Application US/10296734

| Sequence 1471, Application US/10296734
| Publication Wo. US20040054137A1
| GENERAL INFORMATION:
| APPLICANT: Thompson, Scott A
| APPLICANT: Ramshaw, Ian A
| TITLE OF INVENTION: Synthetic molecules and uses therefor FILE REPERENCE: Savine
| CURRENT FILING DATE: 2003-08-04
| PRIOR APPLICATION NUMBER: US/10/296,734
| CURRENT FILING DATE: 2000-05-26
| NUMBER OF SEQ ID NOS: 1507
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 1471
| LENGTH: 1006
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OTHER INFORMATION: X = unknown amino acid
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LOCATION: (38)...(39)
OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: POL Consensus
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NAME/KEY: MISC_FEATURE
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ORGANISM: Artificial
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OTHER INFORMATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (335)(335) OTHER INFORMATION: X = 1	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (365)(365) OTHER INFORMATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (369)(369) OTHER INFORMATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (373)(373) OTHER INFORMATION: X = v	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (402)(403) OTHER INFORMATION: X =	: MISC FEATURE : (434)(434) FORMATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (439) OTHER INFORMATION: X =		FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (470)(470) OTHER INFORMATION: X =	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (480)(480) OTHER INFORMATION: X =	FEATURE: NASC_FEATURE LOCATION: (487)(487)	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (514)(514) OTHER INFORMATION: X = 1	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (534) (535) OTHER INFORMATION: $X =$	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (544)(544) OTHER INFORWATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (553)(553)	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (558)(558)	FEATURE: NAME/KEY: MISC_FEATURE LOCATION: (593)(593) OTHER INFORMATION: X =	FEATURE: NAME/KEY: MISC FEATURE LOCATION: (610)(610) OTHER INFORMATION: X =

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AAGAAGAGCGTGACCGTGCTGGACGTGGGGGGCGTACTTCAGCGTGCCCCTGGACGAG 1038
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                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                   acid
                   amino
                   unknown
                                         4.62e-150
3251.50
88.81%
85.36%
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (675)..(675)
OTHER INFORMATION: X = U
FEATURE:
                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1333 ANGARGCCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
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                ATCGGCCCCACCCCCGTGAACATCATCGCCCGCAACATGCTGACCCAGCTGGGCTGCACC
                              -----SerLeuPheGlyAsnAspProSerSerGlnMetAla----
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               AND
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF
TITLE OF INVENTION: MODIFICATIONS
FILE REPERENCE: 20747Y
CURRENT PEDLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR PELLING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28661
PRIOR APPLICATION NUMBER: 60/217,814
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR PILING DATE: 2001-09-07
PRIOR PLING DATE: 2001-09-07
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
NUMBER: 60/233,180
PRIOR PILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FSSISEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 1350
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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    Command line parameters:
-MODEL=frame+ in 2p. model - DBV=xlh
-MODEL=frame+ in 2p. model - DBV=xlh
-MODEL=frame+ in 2p. model - DBV=xlh
-Lognz_1/USPTO spool/US09610313/runat_31052005_155136_15139/app_query.fasta_1.7893
-DB=A, Geneseq_16Dec04 - QFMT=fastan - SUPFIX=n2p.rag - MINNATCH=0.1 - LOOPCL=0
-LIST=A, DOCALIGN=200 - THR SCORE=pert - THR MAX=100 - THR MIN=0
-LIST=A, DOCALIGN=200 - THR SCORE=pert - THR MAX=100 - THR MIN=0
-USBE-BCOAL - OUTPMT=pco - NORM=ext - HEAPSIZE=500 - MINLEN=0 - MAXLEN=200000000
-USBE-US09610313 @CGN 1 1_557 @runat_31052005 155136_15139 - NCPU=6 - ICPU=3
-NO_WMAP - LARGEQUERY - NEG SCORES=0 - WAAT - DSPBELOKE=100 - LONGLOG
-DBV TIMEOUT=120 - WARN TIMEOUT=30 - THERAPSIZ=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Adp84803 HIV-1 hyb
Adn36406 Human pro
Aab69289 HIV-1 non
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Aab69287 HIV-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4211384
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                             protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
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Listing first 45 summaries
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Post-processing:

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Delivering exogenous (e.g. CFTR) genes to epithelial cells in the respiratory tract using a penetration agent and a lentiviral packaging system, useful for treating e.g. cystic fibrosis.
WPI; 2004-191004/18.
N-PSDB; ADS19485.
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Disclosure, Fig 16; 45pp; English

The present invention relates to a method or delivering one or more exogenous genes for expression of the gene in the expiratory of a mammal to give persistent expression of the gene in the epithelial cell, using a lentiviral packaging (expression vector) system.

Also disclosed are (la a recombinant lentiviral packaging system , comprising a flag protein, and a second nucleic acid molecule including a gag gene sequence encoding a Gagpol protein (the gagpol gene sequence encoding a Gagpol protein (the gagpol gene sequence condition and sequence encoding a Gagpol protein (the gagpol gene sequence conditions) which switches expression of the correct the chance of a frame shift which switches expression of the correct encode either the gag gene or the gagpol gene of cagpol protein to the Gag protein in wild type lentiviral vector nucleic acid molecule which does not encode either the gag gene or the gagpol gene of coord, and (ii) a recombinant nucleoted changes in the frame shift capped and which does not encode either the gag gene or the gagpol gene of which which switches sexpression of the Gagpol protein to the Gag protein in the wild type lentivirus. The exogenous gene is expressed in sufficient numbers of condition. The exogenous gene is exprise fibrosis transmembrane conductance regulator (CFTR) and the condition is cystic fibrosis conductance regulator (CFTR) and the condition is cystic fibrosic tential differentiated and is capable of differentiating into 2 or difference has additionally degenerate nucleocide substitutionally degenerate nucleocide substitutionally degenerate nucleocide substitution which the frame shift event. The gag gene is a truncation of the wild type gagol gene so that it can longer be translated to form Gagpol. The method and recombinant lentiviral packaging system may be used for delivering nucleic acids to epithelial cocidies of a mammal. In particular they may be used to delivery of a non-toxic amount of the resembration. gene for the treatment of CF. It has been found that the delivery of a recombinant lentivirus carrying an exogenous gene to the respiratory system, following the delivery of a non-toxic amount of a penetration enhancer can provide persistence of expression of a gene product. The present sequence represents modified HIV-1 GagPol protein. The present invention relates to a method of delivering one or more

Sequence 1435 AA

								69	382	129	402	189	422
	1435	869	44	40	6	r3		13 ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGC	:::	 70 TTCAAGGGCCCCAAGGGGATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCC	::: :::::::::::::::::::::::::::::::	130 CGCAACTGCCGCGCCCCCCAAGAAGGCCTGCTGGAAGTGCGGGAAGGAGGGCCACCAG 189	:::
	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	16 (1-1435)	ccaccagcgccaac	[alThrAsnSerAlaThr	TCAAGTGCTTCAACTGC	:::::: ArgLysThrValLysCysPheAsnCys(AGAAGGCTGCTGGAAG	
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•	Alignment Scores: Pred. No.:	re:	Percent Similarity:	Best Local Similarity:	Query Match:		US-09-610-313B-32 (1-2457) x ADS19486 (1-1435)	13 ATGGCCG	363 LeuAlaG	70 TTCAAGG	111::: 383 PheArgAe	130 CGCAACTC	::: 403 LysAsnCys
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ATGAAGGACTGCACCGAGG	
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GTG ::: Ile	GGCGGCCAGATCAAGGAGCCCTGCTGGACACCGGCGCCGACGACGACCGAC
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ry = A	997GCGCCAGTACGACCAGATCCTGATCTGCGGCAAGAAGGCCATCGGCACC 597
Va_G	GGTGATCGGCCCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGC 657 :::
ይተ	CACCCTGAACTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGC 717
A—A	GGACGGCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACC 777
g g	CATCTGCGAGGAGATGGAGAGGGGCAAGATCACCAAGATCGGCCCCGAGAACCCC 837
주=2	CAACACCCCCGTGTTCGCCATCAAGAAGAAGAACAGCACCAAGTGGCGCAAGTGGTG 897
A — G	CTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCC 957
5=≅	CCCCGCCGGCCTGAAGAAGAAGAGCGTGACCGTGCTGGCTG
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#=#	CAACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGC 1137
s = 8	CCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCGCAC 1197 ::
임프램	CGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATC 1251 ::::::
ß	GGCCAGCACCGCGCCAAGATCGAGGAGCTGCGGAACCTGCTGCTGCGGCTTCACC 1311

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US-09-610-313B-32 (1-2457) x ADP84803 (1-3183)
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Best Local Similarity:
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DB:
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                                                                 CCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGGTGGACCGTGAAC 1425
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ArgThrArgGlyAlaHisThrAsnAspValLysGlnLeuThrGluAlaValGlnLysIle 962
ACCCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCTG------CCCATCGAGCTGCAC
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mammal an immune response directed to a virus, preferably Human mammal an immune response directed to a virus, preferably Human mammal an immune response directed to a virus, preferably Human (mammalericiency virus (HIV). The method comprises sequentially and recombinant administering to the mammal one or more sequential doses of a recombinant plasmid vector or recombinant viral vector or its derivative, into which the mucheic acid molecules encoding all, part or a modified form of two or more antigens of the virus are incorporated, and one or more optimized CpG motifs, where the antigens have been rendered substantially non-pathogenic. The invention further comprises: a method of vaccinating or preventing viral infection in a mammal; a method of vaccinating or preventing viral infection in a mammal; a wethod of vaccinating a mammal against a viral pathogen; a method of eliciting or inducing an immune response directed to a virus comprising the recombinant viral vector or its functional derivative; a combinant viral vector or its functional derivative; a combinant viral vector or recombinant viral vector; a plasmid vector; a plasmid vector or recombinant viral vector; a plasmid vector; a plasmid vector or recombinant viral vector; a plasmid vector; and recombinant viral vector or recombinant viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eliciting; inducing; immune response; HIV; antigen; non-pathogenic; vaccination; vaccine; HIV-I.
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1143 IleArgLysValLeuPheLeuAspGlyIleAsp 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV-1 hybrid isolate pNL4-3 protein.
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                                                                                                                                                                           ADP84803 standard; protein; 3183
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17-SEP-2003; 2003AU-00905067.
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                                                                                                                                                                                                                                                              ADP84803;
                                                                              RESULT 2

ADPR 4803

ADPR 4803

ADPR 4803

ADPR 4803

ADPR 4803

ADPR 4803

ADPR 52-6

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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

1.47e-205 3701.50 86.96% 81.84% 81.26%

Percent Similarity: 91.36\$ Conservative: 28 Best Local Similarity: 87.86\$ Mismatches: 47 Query Match: 80.54\$ Indels: 23 BB: Gaps: 5 US-09-610-313B-32 (1-2457) x ADN36406 (1-1457)	<u>a</u> —5	Qy 73 AAGGCCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGCCACATCGCCCGC 132	Qy 133 AACTGCCGCGCCCCCGCAAGAAGGCTGCTGGAAAGTGCGGCAAAGGAGGCCACCAGATG 192	Qy 193 AAGGACTGCACCGAGCCCAACTTCTTCCGCGAGGACCTGCCTTCCCCAGGC 252	Qy 253 AAGGCCGGGAGTTCCCCAGCGAGCAGCGCGCCAACAGCCCCACCAGCGGGGTGG 312	Qy 313 CAGGGGGGGGGACAACCCCGGAGGGGGGGGGGGGGGGG	Qy 373 TTC	Db 501 rSerLeuLysSerLeuPheGlySerAspProLeuSerGlnProGln1leThrLeuTrpGl 521	Qy 396 GCGCCCCTGGTGAGCATCAAGGTCGGCCGGCAGATCAAGGAGCCCTGCTGCACACCGG 455 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 456 CGCCGACGACGACGAGGAGGAGGATGAGCCTGCCCGGCAAGTGGAAGCCCAAGATGAT 515	535	557	Qy 576 CGCCAAGAAGACGCCACCGTGCTGATCGGCCCCACCCCGTGAACATCATCGGCCG 635	Qy 636 CAACATGCTGACCCGGCTGCACCCTGAACTTCCCCATCAGCCCCATCGAGACCGT 695	597 gAsnMetLeuThrdlnLeudlyCysThrLeuAsnPheProlleSerProlleGluThrll	Oy 696 GCCCGTGAAGCTGAAGCCCGCCATGGCCCCCAAGGTGAAGCAGTGGCCCCTGACCGA 755 :	Qy 756 GGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGAGGAGAGAGA	816 CAAGATCGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAGACAGAGAGAG	876 CACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG	Db 677 rThrLygTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGLnAspPheTr 697 Qy 936 GGAGGTGCAGCTGGGCATCCCCCACCCGGCCTGAAGAAGAAGAAGAGGTGACCGT 995
	Oy 2062 AGCCTGACCGGAGCCACCAACCGAGCTGCAGCCATCCAGCTGGCCTGCAG 2121	Qy 2122 GACAGCGGCGAGGTGAACATCGTGACAGCCGACAGCCCTGGGCATCATCCAG 2181 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 2182 GCCCAGCCCGACAAGAGCGAGGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAG 2241	Oy 2242 AAGGAGAAGGTGTACCTGAGCTGCCCGCCCACAAGGCATCGCGGCAACGAG 2301	Oy 2302 ATCGACAAGCTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358 :::	RESULT 3 ADN36406 ID ADN36406 standard; protein; 1457 AA.	XX ADN36406;	DT 15-JUL-2004 (first entry)	DE Human protein for anti-HIV vaccine. XX XX anti-HIV; vaccine; HIV; promoter; viral particle; immunization.	AA Homo sapiens. XX By WARDARDERAS		XX PF 17-OCT-2003, 2003WO-US033112.	PR 18-OCT-2002; 2002US-0419465P. XX PA (AARO-) AARON DIAMOND AIDS RES CENT.	XX PI Huang Y, Ho DD, Chen Z; XX	DR WPI; 2004-348328/32. DR N-PSDB; ADN36405.	XX PT Nucleic acid vector comprising at least one HIV sequence operably linked PT to a promoter and encoding a protein that does not assemble into viral PT particles, useful in immunising a subject against HIV infection.		CC The invention relates to a nucleic acid vector comprising at least one CC HIV sequence operably linked to a promoter and encoding a protein that CC does not assemble into viral particles. The nucleic acid vector is useful CC in immunizing a subject against HIV infection. This sequence corresponds		Alignment Scores: Pred. No.: 1e-203 Length: 1457 Score: 3668.50 Matches: 702

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The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B soluties. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-subtype B; gag; pol; env; vpu;
                                      CCAGCCCGACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAA
                                                                                                                                                                                                                                            GGAGAAGGTGTACCTGAGCTGCCCCCCCCACAAGGGCATCGGCGGCAACGAGCAGAT
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Matches:
Conservative:
Mismatches:
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nucleotide sequence.
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vif; vpr; t
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                                                                                                                                           B; gag; pol; env; vpu;
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Novel genomic nucleic acids of non-subtype B human immunodeficiency virus type 1 useful for detecting and treating AIDS comprises a specific
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Mismatches:
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                                                                                       CGCCTGCCCATCCAGAAGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACC
                                                                                                                                                                                                                                                                                                                                           GlySerGluValAsnIleValThrAspSerGlnTyrAlaLeuGlyIleIleGlnAlaHis
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                                                                          CTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATC
                                                                                                                          CAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTG
                                                                                                                                         GlnLysGlnGlyHisAspGlnTrpThrTyrGlnIleTyrGlnGluProPheLysAsnLeu
                                                                                                                                                                           AAGACCGGCAAGTACGCCAAGATGCGCACCCCCACACCACCACGACGTGAAGCAGCTGACC
                                                                                                                                                                                         GAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGGCAAGACCCCCAAGTTC
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The invention relates to molecules comprising HIV-1 subtype isolate regulatory/accessory genes (tat, nef and rev genes) and modifications and derivatives thereof. The invention also provides proteins encoded by such genes. Sequences of the invention are useful for manufacturing vaccines for treating or preventing human immunodeficiency virus (HIV) infections. They are also useful in gene therapy. The present sequence is HIV-1 subtype C isolate Dulis reverse transcriptase (RT) protein. (Updated on 23-0CT-2003 to standardise OS field)
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                               comprising HIV-1 subtype isolate regulatory/accessory for manufacturing a vaccine for treating or preventing
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                                           Disclosure; Page 94-97; 97pp;
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Best Local Similarity:
Query Match:
DB:
WPI; 2003-430497,
N-PSDB; AAD29258
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induction of specific humoral and cellular immune responses. (I) and polypeptides (II) encoded by them, are useful in pharmaceuticals, vaccines and diagnostic agents, particularly for treatment or prevention of human immune deficiency virus-I (HIV-I) infections, also for rational design of test or therapeutic reagents, or gene therapy vectors. Polypeptides, especially antibodies, specifically directed against (II) are since similarly useful as pharmaceutical and diagnostic agents. (I) are specific for intersubtype C/B' of HIV-1 so are useful in regions (particularly China and South-East Asia) where this subtype is prevalent. The products of the invention have antiviral activity. This sequence represents a protein encoded by the HIV-1 subtype C genome described in the method of the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                 GGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCCGCAA 134
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|LeuGlnGlyPro***GluLysGlyLeuLeuGluMetTrpLysArgArgThrProAsnGlu
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Best Local Similarity:
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                                                      AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACC
                                                                                                    GAGACCACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGC
                                                                                                                                                  AGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCCAGGCC
                                                                                                                                                                                                                                               This invention describes a novel polynucleotide isolated from human immunodeficiency virus type 1 subtype C/B' which can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infection; diagnosis; human; humoral immune response; antiviral; cellular immune response; vaccine; treatment; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences from a human immune deficiency virus intersubtype, useful for treatment, prevention and diagnosis of
                                                                                                                                                                                                                                                                                              CTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGCCATCGAT 2358
                                                                                                                                                                                                                                                                                                        codon"
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      1013 tGluGly1leVal11eTrpGlyLysThrProLysPheArgLeuProl1eGlnLysGluTh
                        CTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGT
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Misc-difference 72
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Misc-difference 58
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Misc-difference 114
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GGAGGGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCAT
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                                             CAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCG
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                                                                                                                                                                                              The present invention relates to a process for the selection of human immunodeficiency virus (HIV) subtype isolates for use in the development of a prophylactic and/or therapeutic pharmaceutical composition. The process involves selecting isolated virus or viruses with a high sequence identity to a consensus sequence and a phenotype which is associated with transmission for the particular HIV subtype. The composition can be used in the production of vaccines against HIV. The present sequence is the HIV-1 subtype C isolate Dul51 pol protein. (Updated on 29-AUG-2003 to
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                                                                                                                     Selecting HIV-1 subtype C isolates, which are useful in developing vaccines against HIV infection, comprises isolating viruses with high sequence identity to a consensus sequence whose phenotype is associated
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                           Claim 19; Page 67; 69pp; English
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                                                                  Swanstrom RI,
   15-SEP-2000; 2000ZA-00004924
                        MEDICAL RES COUNCIL
                                             UNIV NORTH CAROLINA
                                   CAPE TOWN
                                                                                                                                                                                                                                                                             HIV-1 subtype C isola
standardise OS field)
                                                                                                                                                       with the HIV subtype.
                                                                                       WPI; 2002-171700/22.
N-PSDB; AAL41592.
                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                          Sequence 854 AA;
                                                                 Williamson C,
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Pred. No.:
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ThriysTrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrp 240
                                                         The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev, and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                            TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCCAGCGAGCAG
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  1 useful for detecting and treating AIDS comprises a specific
                                                                                                                                                                                                     1000
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Conservative:
Mismatches:
Indels:
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                                  Claim 41; Fig 15; 131pp;
              nucleotide sequence.
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                                                                                                                                  rAspTyrTrpGlnAlaThrTrp1leProGluTrpGluPheValAsnThrProProLeuVa
nGluProPheLysAsnLeuLysThrGlyLysTyrAlaLysArgArgThrThrHisThrAs
                                    GGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGAC
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               GCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGGCATCCGCTACCAGTACAACGTG
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This is the amino acid sequence of the pol protein of lymphadenopathy associated virus LAV.MAL (CNCM I-641), a new virus isolate from Zaire that is responsible for diseases clinically related to AIDS. The sequence was deduced from an open reading frame (ORF) of the LAV.MAL genome (see AAV63467). 7 ORFs (see AAW72992-98) were identified. Specific peptides of the envelope glycoprotein can be used as antigens in a claimed method for the in vitro detection of an antibody directed against LAV. The method is useful for the diagnosis of AIDS or pre-AIDS, or to detect antibodies in patients, asymptomatic carriers and in blood-related products. LAV viral for detecting LAV.MAL; HIV; human immunodeficiency virus; diagnosis; vaccine; AIDS; pol. method and ä

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useful in vaccines. (Updated
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                 CGCAGCGAGGCGGCGGAGGGCCAGGGCACCTG-----AACTTCCCCCAGATCACC
                            CTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGCCAGATCAAGGAGGCCCTGCTG
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       CAGGCCCAGCCCGACAAGAGCGAGGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATC
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                                                      immunodeficiency virus; HIV; pol; immunotherapy; infection;
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                                                                                  CAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT
                                                                                                                                                                                                                                                                                                                                                                                                       Novel synthetic therapeutic peptide compounds useful for inducing a immune response in a mammal, specifically cross-react with HIV IV9 epitopes.
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                                                                                                                                        protein;
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                                                                                                                                                                                                                           epitope; vaccine; enzyme.
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                          TrpAlaSerGinileTyrProGly1leLysValArgGinLeuCysLysLeuLeuArgGly
                                       GCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAG
                                             ThrbysAlaLeuThrGluVallleProLeuThrGluGluAlaGluLeuGluLeuAlaGlu
                                                         AACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTG
                                                               GTGGCCGAGATCCAGAAGCAGGCCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCC
                                                                                 ATCGTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCC
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The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a nucleic acid used in the invention.
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for anti-HIV vaccine
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                                                                       Human immunodeficiency virus
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                                 anti-HIV; vaccine; HIV;
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N-PSDB; ADN36412.
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ADN36413 standard; protein; 1003

1		1816 ACCCCAAGTTCCGCCTGCCCATCCAGAAGAGACCTGGGAGACCTGGTGGACGACTAC 	1876 TGGCAGGCCACCTGGAGTCCCCGAGTGGGAGTTCGTGAACACCCCCCCC	1936 TGGTACCAGGAGAAGCAGCCATCATCGGCGCGAGACCTTGTAGGTGGACGCGCCCCCCCC	1996 GCCAACCCCAGACCCACAATCGGCAAGGCCGGCTACGTGACCGACC	2056 ATCGTGACCTGACCACCACCACAAGACCAGAGGCTGCAGGCCATCCACTGGCC ::: :::		2176 ATCCAGGCCCAGCCGACAAGAGGGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTG	Qy 2236 ATCAAGAAGGAGAAGGTGTACCTGAGCTGGCCGCCCCCCACAAGGCCATCGGGGGAAC 2295	Oy 2296 GAGCAGATCGACAGGGGGGCATCCGCAAGGTGCTGTTCCTGGACGCATC 235:	Oy 2356 GAT 2358 Db 721 Asp 721	RESULT 14 AAP81861 ID AAP81861 standard; protein; 1002 AA.	AC AAFS1801; XX XX DT 27-AUG-2003 (revised) DT 25-MAK-2003 (revised) DT 55-MAK-2003 (first entry)	sence encoded by LAV MA L PO	XX	PN WO8707906-A. XX XX PD 30-DEC-1987. XX
568 GAGATCTGCGGCAAGAAGCCATCGGCACCGTGATCGGCCCCACCCCGTGAACATC 627	IleGlyArgAsnLeuLeuThrGln1leGlyCysThrLeuAsnPhePro1leSerPro1le GaGACCGTGCCCGTGAAGCCCGGCATGGACGCCCCCAAGGTGAAGCAGTGGCCC	101 GIUINIYAIFIOVAILYBEHGULYSFIOG-IYMEKASDGIJYFIOLYBVAILYBGINIIDFIO 180 748 CTGACCGAGGAAAGATCAAGGCCTGACCGCCATCTGCGAGGAGAAGAAGGAGGC 807	AAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGGGTTCGCCATCAAGAAG	868 AAGGACAGCAACGAGGCGGAAGCTGGTGGACTTCCGCGAGCTGAACAAGGGCACCCAG 927 	928 GACTICTGGGAGGGGGGCTGGGCATCCCCCGCCGCCGGCTGAAGAAGAAGAAGAGC 987 	988 GTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGC 1047 	1048 AAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGCACCCCGGCATCCGCTACCAG 1107 		A AGATCCTGGAGCCTTCCGGGCCCGCACCCCGAGATCGTGATCTACCAG	CCCTGTACGTGGGCAGCGACTGGAATCGGCCACGCGCGCCACAATCGAGGAGCTG ASDLeutyvya, G1985 T885 Leutill	CGCAGAGCACCTGCTGCGCTGGGGCTTCACCACCCCCGACAAGAACCAGAAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCACCAGAAGCAGAAGCTTCACCACCAGAAGAAGTTCACCACAAAGAAGTTCACAAAAGAAGATAAAGAAGAAGAAGAAGAAGAAGAAGAAGAA		1396 CTGCCCGAGAAGGAGGCTGGACCGTGAACAACATCCAGAAGCTGGGCAAGCTGAAC 1455 	1456 TGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGG 1515 	1516 GCCAAGGCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAG 1575 	1576 AACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCAAGGACCTG 1635

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LAV EL I (AAN80436) and LAV MA L (AAN80437) were isolated from the peripheral blood lymphocytes of patients. Different AIDS virus isolates concerned are designated by 3 letters of the patients name. Stable probes including the DNA sequences can be used for detection of the new LAV viruses or related viruses or DNA proviruses in eg. biological samples. The proteins or peptides can be used for detection of antibodies induced in vivo and present in biological fluids. The DNA can also be used for the expression of LAV viral antigens for the prodn. of a vaccine against the detection of proteins related to the LAV viruses, partic. for diagnosis of AIDS or pre-AIDS. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct PI
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GlnLeuThrGluAlaValGlnLysIleAlaGlnGluSerIleValIleTrpGlyLysThr
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                                                                          GInAlaThrTrpIleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrp
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The specification describes a method of determining the influence of variation in host genes on selection of microorganisms with protein substitutions. The method comprises typing all individuals of a substitutions. The method comprises typing all individuals of a population of patients infected with a microorganism for at least one selected intrinsic polymorphic marker involved in the host response to the presence of the microorganism. The method is useful for examining selective pressures confronting a wide range of organisms that exhibit pathogenic traits in a host, such as bacteria, improbacterium, viruses and virus-like particles; for examining microorganisms that have adapted to evolve rapidly, including HIV and AIDS related viruses and the heptitis related viruses such as HCV and HBV. The method is useful for designing a vaccine to prevent or delay the emergence of drug resistence in patients treated with a particular drug specific for a microorganism at the nucleotide or amino acid level. The present sequence represents a HIV pol protein, which is expected to provide optimal cytotoxic T lymphocyte (CIL) induced therapeutic protection to the cohort examined in that study
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AAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAG

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Claim 22; Page 88-89; 157pp; English.

FBIleGlyProGluAsnProTyrAsnThrProValPheAlaIleLysLys 220	CAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAG 927	GACTTCTGGGAGGTGCAGCTGGGCATCCCCCGCCGGCCTGAAGAAGAAGAAGAGC 987	TGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCCTGGACGACTTCCGC 1047	AAGTACACCGCCTTCACCATCCCCAGCATCAACAACAACCAGCCATCCGCTACCAG 1107	TACAACGTGCTGCCCCAGGGCTGGAAGGCCAGCATCTTCCAGAGCAGCATGACC 1167	CCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCTACCAGGCC 1221	CCCCTGTACGTGGGCAGCCAGCAGAGATCGGCCAGCACCGCCAAGATCGAGGAGCTG 1281	CGCAAGCACCTGCTGCGCTGGGGCTTCACCACCCCGACAAGAAGCACCAGAAGGAGCCC 1341 ::: :::	CCCTTCCTGCCCATCGAGGTGCACCCGGACAGACGGAGCGGCGCCATCGAG 1395	CTGCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAAC 1455 LeuProGluLy8AspSertrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsn 420	TGGGCCAGCCAGCTCTACCCCGGCATCAAGGTGCGCCAGCTGCTGCAAGCTGCTGCGCGGC 1515	GCCAAGGCCCTGACCGACTTCGTGCCCCTGACCGAGGCCGAGGCTGGAGGTGGCCGAG 1575	AACCGCGAGATCCTGCGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCAAGGACCTG 1635 	GTGGCCGACATCCACAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCC 1695 :::	TTCAAGAACCTGAAGACCGGCAAGTACGCCACGCGCCCCCACCCA	AAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGGCGTGATCTGGGGGAAG 1815 	ACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTAC 1875	TGGCAGCCACCTGGATCCCCGAGTGGGACTTCGTGAACACCCCCCCC
IleGly	868 AAGGACAGCACCAAGTGGC 	928 GACTTCTGGGAGGTGCAGC 	988 GTGACCGTGCTGGACGTGG 	1048 AAGTACACCGCCTTCACCA 	1108 TACAACGTGCTGCCCCAGG 	1168 AAGATCCTGGAGCCCTTCC 	1222 CCCTGTACGTGGGCAGCG 	1282 CGCAAGCACCTGCTGCGCT ::: ::: 361 ArgGlnHisLeuLeuLysT	1342 CCCTTCCTGCCCA 381 ProPheLeuTrpMetGlyT	1396 CTGCCCGAGAAGGAGAGCT 	1456 TGGGCCAGCCAGATCTACC 	1516 GCCAAGGCCCTGACCGACA :::: 441 ThrLygAlaLeuThrGluV	1576 AACCGCGAGATCCTGCGCG ::: 461 AsnArgGluIleLeuLysG	1636 GTGGCCGAGATCCAGAAGC :::	1696 TTCAAGAACCTGAAGACCG	1756 AAGCAGCTGACCGAGGCCG 	1816 ACCCCCAAGTTCCGCCTGC 	1876 TGGCAGGCCACCTGGATCC

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A;Accession: S54378
A;Status: preliminary
A;Molei type: genomic RNA
A;Residues: 1-1002 <THE>
A;Cross-references: UNIPROT: P12499; EMBL:M22639; NID:g329377; PIDN:AAA45366.1; PID:g3293
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
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R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                         protein search, using frame_plus_n2p model
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1002 < SPI>
A; Residues: 1-1002 < SPI>
A; Residues: 1-1002 < SPI>
A; Cross-references: UNIPROT: P18802; GB: M27323; NID: 9328154; PIDN: AAA44869.1; PID: 9328158
C; Comment: Specific enzymatic cleavages may yield mature proteins including protease, references: comparing the cleavages may yield mature proteins including protease, reference: pol
C; Genetics:
A; Genetics:
C; Superfamily: pol polyprotein
C; Superfamily: 
                                                                            ;Superfāmily: pol polyprotein
;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucled
;56-154/Product: retropepsin #status predicted <RTP>
;80/Active site: Asp (shared with dimeric partner) #status predicted
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|IleCysGlyTyrLysAlaMetGlyThrValLeuValGlyProThrProValAsnIleIle
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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75.84%
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8 4 8 4 8 4 8	6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H
	RESULT 3 GANNAL 1 H.V.1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LaV-la) H.V. I retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate LaV-la) H.V. Contains: endonuclases (EC 3.1); rectpepsin (EC 3.4.23.16); RNA-directed DNA poly C. Species: human immunodeficiency virus type 1, HIV-1 C. Anote: host Home spatiens (man) A. Anote: host Home spatiens (man) C. Superiminity Home spatiens (man) C. Superiminity Home spatiens (man) A. Anote: host Home spatiens (man) C. Superiminity Home spatiens (man) A. Anote: host Home spatiens (man) A. An

qq	461 AsnArgGluIleLeuLysGluProValHisGlyValTyrTyrAspProSerLysAspLeu 480	A,Gene: pol
දු පු	1636 GTGGCCGAGATCCAGAAGCAGGGCCACGACCAGCGAGCTACCAGATCTACCAGGAGCCC 1695 :::	C;Reywords ALDS, polyprocein C;Reywords ALDS, aspartic proteinase, endonuclease, hydrolase, immunodeficiency, nucleo F;69-167/Product: retropepain #status predicted <rtp> F;93/Active site: Asp (shared with dimeric partner) #status experimental</rtp>
& g	1696 TTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCACCACGACGACGTG 1755	
දු පු	1756 AAGCAGCTGAGGCCGTGCAGAAGATCGCCATGGAGGATCGTGATCTGGGGCAAG 1815	Percent Similarity: 93.18\$ Conservative: 33 Best Local Similarity: 88.68\$ Mismatches: 30 Query Match: 75.35\$ Indels: 20 DB: 5
8 8		-09-610-313В-32 (1-2457) х GNVWH3 (1-1015)
8 &	541 InfriolysPheLysLeuProlleGinLysGluThritpGluThrTrpTrpTrpTrpTuTgluTyr 560 1876 TGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCC	Oy 220 TTCTTCCGCGAGGACCTGCCCCCAGGCCAAGGCCCGCGAGTTC 267
숨 &	561 TrpdinalaThrTrplieProdluTrpdluPheValAenThrProProLeuValLygieu 580 1936 TGGTACCAGCTGGAGAAGGCCCATCATCGGCGGCCCGAGCCTTCTACGTGGACGCGCC 1995	Qy 268
염 &	581 TrpTyrdlineudluLygdluProllevalGlyAlaGluThrPheTyrValAspGlyAla 600 1996 GCCAACCGCGCAACCCACAACACCCGCCCGCCCGCCCCGCCCCGCCCACAAG 2055	Qy 304 CGCGAGCTGCAGGTGCGCGGCGACAACCCCGCGAGCGAGGCCGGCGGCGGCGG 357
g &	601 AlaSerArgGluThriberGlyLyTHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	Qy 358 CAGGGCACCCTGAACTICCCCCAGATCACCCTGGGGCAGCGCCCCTGGTGAGC 411
g S	640	ATCAAGGTGGGCCGCAGATCAAGGAGGCCCTGCTGGACACCGGCGCCGACGACGACGTG 4
qq		472
oy B	2176 ATCCAGGCCCAGCCAGAGAGCGAGAGCGAGAGCTGATGAACCAGATCATCGAGCAGCTG 2235	Db 101 LeuGluclumetSerLeuProGlyArgTrpLy8ProLy8MetIleGlyGlyIleGlyGly 120 Qy 532 TTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATC 591
ò.	atcaagaagaagaaggggggggggggggggggggggggg	
8 &	681 IleLysUysGluLysValTyrLeuAlaTrpValProAlaHisLysGlyIleGlyGlyAsn 700 2296 GAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGCATC 2355	Qy 592 GGCACCGTGCTGATCGGCCCCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAG 651
ය පි	701 GluGlnValAspLysLeuValSerAlaGlyIleArgLysValLeuPheLeuAspGlyIle 720 2356 GAT 2358	Qy 652 CTGGGCTGCACCCTGAACTTCCCCATCGAGACCGTGCCCGTGAAGCTGAAG 711 ::
	721 Asp 721 4	Qy 712 CCCGGCATGGACGCCCCAAGGTGAAGCAGTGGCCCCTGACCGAGAGAGA
GNVWH3 HIV-1 rc N;Conta: C;Specie	etropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (isolate HTLV-III ins: endonuclease (EC 3.1); retropepsin (EC 3.4.23.16); RNA-directed DNA polyes: human immunodeficiency virus type 1, HIV-1	Qy 772 CTGACCGCCATCTGCGAGGAGGAGGAGGCAAGATCACCAAGATCGGCCCGGG 831
A) Note: C; Date: C; Acces R; Ratne:	A;Note: 109t note Saptens (wan) C;Date: 109t note Note Saptens (wan) C;Accession: A03965 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A03965 R;Ratner, L.; Haseltine, W.; Patarcac, R.; Livak, K.J; Starcich, B.; Josephs, S.F.; Dora Rherder, J.A.; Panas, T.S.; Ghraveh, J.; Chang, N. T.; Gallo, D.; Wonn-stan)	Oy 832 AACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAACACACAC
Nature A; Title A; Refer	313, 277-284, 1985 : Complete nucleotide sequence of the AIDS virus, HTLV-III. ance number: A93383, MUID:85111123, PMID:2578615	Qy 892 CTGGTGGACTTCCGCGAGCTGAACAACGCACCCAGGACTTCTCGGAGGTGCAGGTGCAGC 951 Db 241 LeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluValGlnLeuGly 260
A, Molec A, Residi	lle type: DNA Las: 1-1015 <rat> -references: UNIPROT:P03366; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326</rat>	Qy 952 ATCCCCACCCGCCGCCTGAAGAAGAAGAAGACGTGACCGTGCTGGACGTGGCGAC 1011
C;Comme C;Genet	nt: Specific enzymatic cleavages may yield mature proteins including protease, relics:	1012 GCCTACTTCAGCGTGCCCCTGGACGAGCACTTCCGCAAGTACACCGCCTTCACCATCCCC 1

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0 3 4 4 4 4 4 5 5 6 6 6 6 6 6 7 7 8 6 6 7 7 8 6 7 7 7 8 7 8	ACATGCTGACCCAGGTGGGCTGCACCTGAACTTCCCCATCAGCCCCATC 687 ::: :::	GCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAACAGTGGCCC 747 	AGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAGAGGGC 807 	AGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAG 867 	CCAAGTGGCGCAAGCTGGGGACTTCCGCGAGCTGAACAAGCGCACCCAG 927 	AGGTGCAGCTGGGCATCCCCCCCCCCCCCCCCGAAGAGAAGAAGAGC 987 	TGGACGTGGCCGACCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGC 1047 	TTCACCATCCCCAGCATCAACAACGAGCACCCCGGGATCCGGGTIIIIIIIIII	CCAGCATCTTCCAGA(::: roAlaIlePheGInS	CCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCTACCAGGCC 1221 ::: :::	CCCIGTACGIGGGGAGGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTG 1281 		CCCATCGAGCTGCACCCCGACAAGTGGACCGTGGAGCCCATCGAG 1395 	AGGAGAGCTGGACCTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAAC 1455 :::	CAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGC 1515	Н 4	TCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTG 1635 :::	GTGGCCGAGATCCAGAAGCAGGCCACGACCACGAGCCTACCAGATCTACCAGAGCCC 1695
	28 ATCGGCCGCAACATGCTGACCCAGCTG	88 GAGACCGT 6 61 GluThrVa	48 CTGACCGAGGAGAAGATCAAGGC 	08 AAGATCACCAAGAT ::: 01 LysileSerLysil	8 AAGGACAGCACCAAGTGGGGCAAGCTGC	8 GACTTCTGGGAGGTG 	8 GTGACCGTGCTGGAC 	8 AAGTACACCGC 1 LysTyrThrAl	08 TACAACGTGCTGCCCCAGGGTGGAAGGGCAGCC 	8 AAGAT 1 Lysil	2 C	2 4	2 CCCTTCCTG 1 ProPheLeuTrp	6 CTGCCCGAGAAGGA :: 1 LeuProGluLysAs	6 TGGGC 1 TrpAl	6 GCCAA	6 AACCG 1 AsnAr	v

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                                                1756 AAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGGAGCATCGTGATCTGGGGCAAG
                                521 LysGlnLeuThrGluAlaValGlnLysIleAlaAsnGluSerIleValIleTrpGlyLys
                                                                         2116 CTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATC
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HIV-1 retropepsin (EC 3.4.23.16) - human immunodeficiency virus type 1 (strain YU-2) M;Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly. C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) (C;Date: host Homo sapiens (man) (C;Date: 31-Dec-1993 #text_change 09-Jul-2004)

CiAccession: B44001

Rili, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

N. Virol. 66, 6587-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Recession: B44001

A;Rocession: B44001

A;Rocession: B44001

A;Rocession: B44001

C;Comment: This protein is synthesized as a gag-pol polyprotein.

C;Comment: Specific enzymatic cleavages may yield mature proteins including proteinase, C;Genetics:

C;Superfemily: pol polyprotein C;Superfemily: aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo F;S7-155/Product: retropepsin #status predicted <RTP> F;81/Active site: Asp (shared with dimeric partner) #status predicted

1222 CCCCTOTA COTOCOCCOCCOCCOCCOCCOCCOCCCCCCCCCC
6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
Address

Score: Score: Percent Similarity: 93.12\$ Conservative: 34 Best Local Similarity: 88.45\$ Mismatches: 30 Query Match: 74.56\$ Indels: 20 Gaps: 15-09-610-313B-32 (1-2457) x GNVWVL (1-1012) Qy 238 GCCTrCCCCAGGGCAAGGCCCGCGAGTTC	4 AlaPheLeuGlnGlyLysAlaArgGluPheSerSerGluGlnThrArgAlaAsnSe	<pre>Qy 268CCCAGCGGGGGAACGCGCCACCACCACCGCGGGGGGGG</pre>	Qy 319CGCGGCGACAACCCCCGCAGCGGCCGGCCCGAGCGCCAGGGCACCCTG 3	Oy 370 AACTICCCCCAGAICACCTGTGGCAGCGCCCCTGGTGAGCATCAAGGTGGGCGCCCAG 4	Qy 430 ATCAAGGAGCCCTGCTGGACACCGGCGCCCACGACACGTGCTGGAGGAGATGAGCCTG 4 :::	Qy 490 CCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAG 5	Qy 550 TACGACCAGATCCTGATCGACATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGC 6	Oy 610 CCCACCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCTGAAC 6	Oy 670 TICCCCATCAGCCCCATCAGACCCGTGAAGCTGAAGCCCGGCATGGACGCCCC 7	Oy 730 AAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG 7	Qy 790 GAGATGGAGAAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCC 8	850 GTGTTC 850 H 224 Valphe	Qy 910 CTGAACAAGGGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCGGGGG	Oy 970 CTGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCC 1	Oy 1030 CTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACGAGGACC 1	1090	DD 304 ProgrylleArglyroiniyrABNValbeurrocinosylipbyBolySelFroataire o
Qy 1696 TTCAAGAACCTGAAGACCGGCAAGATACGCCACGCCCACACCAACGACGTG 1755 Db \$01 PheLysAsnLeuLySThrdlyLysTyrAlaArgMetArgGlyAlaHisThrAsnAspVal 520 Qy 1756 AAGCAGCTGACCGAGCCGTGCAGAAGATCGCCATGGAGGATCTGGGGCAAG 1815 Db \$21 LysGlnLeuThrGluAlaValGlnLySValSerThrGluSerTleValIleTTFGlyLyS 540 Qy 1816 ACCCCCAAGTTCGCCTGCCCATCCAGAAGAAGAAGAAGAAGAAGAAGAAGAACCTGGGAGCCTACCAGACCACGACTAC 1875	541 IleProLysPheLysLeuProlleGlnLysGluThrTpGluAlaTrpTrpMetGluTyr 560	Oy 1876 TGGCAGGCCACCTGGATGCGGAGTTCGTGAACACCCCCCCTGGTGAAGTG 1935	Oy 1936 TGGTACCAGCTGGAGAAGCCCATCATCGGCGCGAGACCTTCTACGTGGACGGCGCC 1995	Qy 1996 GCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGAGGCCGGGCCGCAGAAG 2055	Qy 2056 ATCGTGACCTGACCGAGACCACCAAGACCGAGCTGCAGCCATCCAGCTGGCC 2115	Oy 2116 CTGCAGGACAGCGAGGTGAACATCGTGACCGACAGCCCAGTACGCCTGGGCATC 2175	Oy 2176 ATCCAGGCCCAGCCGACAAAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGG 2235	Qy 2236 AICAAGAAGGAGAAGGTGTACCTGAGCTGGGGCCCCCCACAAGGGCATCGGCGGCAAC 2295	Qy 2296 GAGCAGATCGACAAGCTGGTGAGGAAGGGCATCCGCAAGGTGCTGTTCCTGGACGGCATC 2355	Qy 2356 GAT 2358 Db 721 Asp 721		Any Terropepsin (b. 3-1-2-1-0); Tetropepsin (b. 3-1-2-1-0); RNA-directed DNA poly C); Species: human immunodeficiency virus type 1, HIV-1 C)species: human immunodeficiency virus type 1, HIV-1 C)species: humay-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C)Accession: A03967	R;Mucsing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. Nature 313, 450-488, 1985 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi A;Reference number: A93355; MUID:85111157; PMID:2982104	A,Accession: A03967 A,Molecule type: DNA A,Residues: 1-1012 <mue> A,Crose-references: UNIPROT:P03368</mue>	cluding protease	C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucled F;66-164/Product: retropepsin #status predicted <rtp> F;90/Active site: Asp (shared with dimeric partner) #status experimental</rtp>	Alignment Scores: Pred. No.: 4.53e-151 Length: 1012

8 8	RESULT 9 GNLJSI HIV-1 retropepsin (EC 3 N.Contains: endonucless	C;Species: simian immur A;Note: host Pan trog1 C;Date: 30-Sep-1991 #se	Riffuet, T.; Cheynier, R. Nature 345, 356-359, 19 A.Title: Genetic organia A.Reference number: 809	A,Accession: S09884 A,Status: nucleic acid A,Molecule type: DNA A,Residues: 1-1027 <hue< th=""><th>A;Cross-references: UN C;Comment: Specific en C;Genetics: A;Gene: Dol</th><th>C;Superfamily: pol pol C;Keywords: AIDS; aspa F;81-180/Product: retr F;105/Active site: Asp</th><th>Alignment Scores: Pred. No.: Score:</th><th>Percent Similarity: Best Local Similarity: Query Match: DB:</th><th>US-09-610-313B-32 (1-24</th><th>Oy 159 CIGCIGGAA</th><th>Db 7 LeuLeuAla</th><th>Db 27 -PhePheAr Ov 279 GAACCGCGC</th><th>46</th><th>333</th><th>OY 393 GCAGGCCC</th><th>98</th><th>Db 106 rGlyAlaAB</th><th>Qy 513 GATCGGCGG</th><th>Db 126 tiledlydl</th></hue<>	A;Cross-references: UN C;Comment: Specific en C;Genetics: A;Gene: Dol	C;Superfamily: pol pol C;Keywords: AIDS; aspa F;81-180/Product: retr F;105/Active site: Asp	Alignment Scores: Pred. No.: Score:	Percent Similarity: Best Local Similarity: Query Match: DB:	US-09-610-313B-32 (1-24	Oy 159 CIGCIGGAA	Db 7 LeuLeuAla	Db 27 -PhePheAr Ov 279 GAACCGCGC	46	333	OY 393 GCAGGCCC	98	Db 106 rGlyAlaAB	Qy 513 GATCGGCGG	Db 126 tiledlydl
	364 ThrLyslledluGluLeuArgGlnHisLeuLeuArgTrpGlyLeuThrThrProAspLys 383 1324 AAGCCAGAAGGAGCCCCCCCTTCCTGCCCATCGAGCTGCACCAGAGTGG 1377	1378 ACCGTGCAGCCCATCGAGCTGCCCGAGAAGAGAGCTGGACCGTGAACGACATCCAGAAG 1437 	1438 CTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTG 1497 	1498 TGCAAGCTGCGCGCGCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGC 1557 	1558 GAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTACTAC 1617	1618 GACCCCAGCAAGGACCTGGCCGAGATCCAGAAGCAGGCCACGACCAGGGCCTAC 1677 	1678 CAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACC 1737 	1738 GCCCACACCAACGACGTGAAGCAGCTGACCGTGCAGAAGATCGCCATGGAGAGC 1797 	1798 ATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGCTGGGAG 1857		1858 ACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACC 1917 	1918 CCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACC 1977 	TTCTACGTGGACGGCCGCCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACC	lthr	523 ONCONOCIONAL CONTROLLO	2098 CAGGCCATCCAGCTGGCCCTGCAGGACCAGCGAGGAGGTGAACATCGTGACGGCGGGG 2157		664 GlnTyrAlaLeuGlyIleIleGlnAlaGlnProAspGlnSerGluSerGluLeuValAsn 683	2218 CAGATCATCGAGCAGCTGATCAAGAAGAGAGAGAGCTGAGCTGAGCTGGGGTGCCCGCCC
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3.4.23.16) - simian immunodeficiency virus SIVCpz
ase (EC 3.1.-.); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
unodeficiency virus SIVCpz
lodytes (chimpanzee)
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nzymatic cleavages may yield mature proteins including protease, re
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artic proteinase; endonuclease; hydrolase; immunodeficiency; nucleo
ropepsin #status predicted <RTP>
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eGluGlnLeuIleLysLysGluLysValTyrLeuAlaTrpValProAlaHis 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nization of a chimpanzee lentivirus related to HIV-1. 09983; MUID:90259077; PMID:2188136
                                                                                                                                                                                                                                                                                                                                R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
1990
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88.38%
79.86%
69.55%
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RESULT 10
533980
pol polyprotein - human immunodeficiency virus type 1
c;Species: human immunodeficiency virus type 1
c;Species: human immunodeficiency virus type 1
c;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Refatus: preliminary
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A;Residues: 1-912 «CAR»
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        CGTGCCCGTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCTGAC
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octein - human immunodeficiency virus type 1, human immunodeficiency virus type 1, HIV-1 human immunodeficiency virus type 1, HIV-1 - Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000 m: T01668 m: T01668 M:; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P. 3-4, 1986 enetic variability of the AIDS virus: Nucleotide sequence analysis of two isol m: T01668 translated from GB/EMBL/DDBJ

type: mRNA: 1-902 <ALI> erences: BMBL:K03456; NID:g60228; PIDN:CAA28012.1; PID:g60230 lly: pol polyprotein

cores:

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Length: 902 Matches: 570 Conservative: 28 Mismatches: 18 Indels: 2	1-902)	ATGATCGCCGCCATCCGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAG	ATCTGCGGCAAGAAGGCCATCGGCACGTGCTGATCGGCCCCACCCCCGTGAACATCATC	ThrilebeuvalGlyFroin		ACCGIGCCCCTGAAGCTGAAGCCCGCCATGGACGCCCCAAGGTGAAGCAGTGGCCCCTG	ACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGCAAG	ATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCCGTGTTCGCCATCAAGAAGAAG	ProTyrAsnThrProValPhe	GACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGGGAGCTGAACAAGCGCACCCAGGAC	TTCTCGGAGGTGGAGTTGGCTATCCCCCCCCCCCCCCCC		ACCGIGCTGGACGTGGGCGCCTACTTCAGCGTGCCCCTGGACGAGGACTTCCGCAAG	TACACCGCCTTCACCATCCCCAGCATCAACGAGACCCCCGGGCATCCGCTACCAGTAC	cileAsnAsnGluThrProGly	AACGTGCTGCCCAGGGCTGGAAGGGAGCCCCAGCATTTCCAGAGCAGCATGACAAG 	ATCCTGGAGCCCTTCCGCGCCCGCAACCCCGAGATCGTGATCTACCAGGCCCCC	sAsnProGluileValileTy	CTGTACGTGGGCAGCTGGAGATCGGCCAGCACCGGCCAAGATCGAGAGCTGCGG 	AAGACTGCTGCGCTCGGCGTTCACCCCCGGACAAGAGAAGAGGCCCCCC	ThrThrProAspLysLysHi	TTCCTGCCCATCGAGCTGCACCCGACAAGTGGACCGTGCAGCCCATCGAGCTG	CCCGAGAAGGAGGTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGG :::	
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Ching, W.T.; Ho, D.D. S.A. 90, 25-29, 1993 zidovudine-resistant human immunodeficiency virus type 1 in the leic acid sequence not shown; not compared with conceptual tra Н r-sensitive variant - human immunodeficiency virus type ficiency virus type 1, HIV-1 snce_revision 18-Nov-1994 #text_change 09-Jul-2004 2118 CCTGCCCATCCAGAAGAAGACCTGGAGACCTGGTGGACCGACTACTGG 1878 AATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCTGGTGAAGCTGTGG 1938 CTGGTGAGCAAGGCATCCGCAAGGTGCTGTTCCTGGACGGCATCGAT 2358 CGCGAGCCCGTGCACGCGTGTACTACGACCCCAGCAAGGACCTGGTG 1638 AAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTC 1698 ACCGGCAAGTACGCCAAGATGCGCACCGCCCACCAACGACGTGAAG 1758 GCCGTGCAGAAGATCGCCATGGAGGATCGTGATCTGGGGCAAGACC 1818 AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGGCCGGCAGAAGATC 2058 AGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATC 2178 560 580 ||||||||| LysglnglyglnglyglnTrpThrTyrGlnIleTyrGlnGluGlnTyr 400 GACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAAC GAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTG , MUID:93126353; PMID:7678340

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Alignment Scores:

Pred. No.: 4.88e-119 Length: 559 Score: 2708.00 Matches: 506 Percent Similarity: 95.17* Conservative: 26 Best Local Similarity: 90.52* Mismatches: 23 Query Match: 59.45* Indels: 4 DB: 2 Gaps: 2	1621 CCCAGCAAGACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAGTGGACCTACCAG
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1267 AAGATCGAGGAGCTGCGCAAGCACTGCGCTGGGGCTTCACCACCCCGACAAGAAG [RESULT 14 846347 polyprotein - simian immunodeficiency virus SIVagm (isolate SAB-1) C;Species: simian immunodeficiency virus SIVagm
Qy 1327 CACCAGAAGGAGCCCCCTTCCTGCCCATGGAGCTGCACCCCGACAAGTGGACC 1380	A;Variety: isolate SAB-1 C;Dace: 55-Dec-1994 #sequence_revision 14-Feb-1997 #text_change 26-Aug-1999 C;Accession: S46347 R;Jin, M.J.; Hui, H.; Robertson, D.L.; Mueller, M.C.; Barre-Sinoussi, F.; Hirsch, V.M.;
Qy 1381 GTGCAGCCCATCGAGCTGCCCGAGAAGGAGCTGGACCGTGAACGACATCCAGAAGCTG 1440	EMBO J. 13, 2935-2947, 1994 A,Title: Mosaic genome structure of simian immunodeficiency virus from West African grec A;Reference number: S46335; MUID:94298785; PMID:8026477 A;Accession: S46347
Qy 1441 GTGGGCAAGCTGAACTGGGCCAGCAGCTCACCCGGCATCAAGGTGCGCCAGCTGTGC 1500	A;Status: nucleic acid sequence not shown; translation not shown A;Andiecule type: DNA A;Residues: 1-1039 < JIN> A;Residues: 1-1039 < JIN> A;Cross-references: EMBL:104005; NID:9466229; PIDN:AAA21505.1; PID:9466231
Qy 1501 AAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACCCTGACCGAGGAGGCCGAG 1560	Ajexperimental source: isolate about mounty A. Experimental source: isolate about 1993 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993 A;Note: this reading frame extends between two stop codons and does not begin with a stationary and abouties:
Qy 1561 CTGGAGCTGGCCGAGAACCGCGAGAATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGAC 1620 	Alignment Scores: 2.61e-100 Length: 1039

Score: Percent	s: 2307.00 Matches: 436 int Similarity: 73.54 Conservative: 120	qa	318
Best Local Query Match DR.	Similarity: 5/.67% Mismatches: 50.65% Indels:	È	1123
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TACCCGGCATCAAGGTGCGCCAGCTGGCCAGGCGCCAGGCCCTGACC 153 1471 TACCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCGCGCGC	398 ThrTrpGlyPheLysThrProGluLysPheGlnLysAspProProFyrLeuTrpMet 417 1351 CCCATCGAGCTGCACCCGACAAGTGGACCGCCCATCGAGCTGCCCGAGAAGGAG 141 418 GlyTyrdluLeuTyrProLysLysTrpGlnLeuGlnGluIleThrLeuProGluArgGlu 437 1411 AGCTGGACCGTGAAGCACTCCAGAAGCTGGTGGCGCAAGCTGGAACTGGTCAGTC 147 1438 GluTrpThrValAsnAspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIle 457 1471 TACCCGGCATCAAGGTGCGCCAGCTGTGCGGCGCGCGCCCAAGCCCTGACC 153 1471 TACCCGGCATCAAGGTGCGCCAGCTGTGCAGCTGCGCGGCGCAGAGCCCTGACC 153 1531 GACATCGTGCCCCTGACGCGCCAGCTGCTGCCGCGCGCCCAAGGCCCTGACC 153 1531 GACATCGTGCCCCTGACGCGCGGCTGACCTGCCGGGGAGACCGGGGAGATCTG 159 1531 GACATCGTGCCCCTGAGGGCCGAGGCCGAGAACCGCGAGAACCGGGGGTGTGCGGGGCCGAGATCCAG 165 1531 GACATCGTGCCCCTGACGAGGAGCCCAGCAGAACCGGGGAGATCCAG 165 1531 GACATCGTGCCCCTGACGGCGGGCCCAGGAGATCCAG 165 1531 CGCGGCCCGTGCACGGCGGCTGACAGGACCCGGGGGAGATCCAG 165 1531 CGCGGCCCGTGCACGGCCCAGCAAGGACCTGGCGGGGCCGAGATCCAG 165 1531 CGCGGCCCGTGCACGGCCCAGCAAGGACCTGGCGGGGCCGAGATCCAG 165	398 ThrTrpGlyPheLysThrProGluLysPheGlnLysAspProProTyrLeuTrpMet 417 1351 CCCATCGAGCTGCACCCCGACAAGTGGACCCATCGAGCTGCCCGAGAAGGAG 141 418 GlyTyrGluLeuTyrProLysLysTrpGlnLeuGlnGluIleThrLeuProGluArgGlu 437 1411 AGCTGGACCTCCAACACTCCAGAAGCTGGTGGCCAGCTGACCGAGTC 147 438 GluTrpThrValAsnAspIleGlnLysLeuAsnTrpAlaSerGlnIle 457 1471 TACCCGGCATCAAGGTGGCGAGCTGGCGAGCTGCGCGCGAGTC 154 1458 TyrThrGlyIleLysThrLysHisLeuCysArgLeuIleArgGlyAlaArgProLeuThr 477 1531 GACATCGTGCCCTGACGGAGGCGGGCGGGGCCGAGGCCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCGGGGCGGGGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCCGAGCTGGCCGAGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCCGAGGTGGCTGGCCGAGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCCGAGGTGAGCTGGCCGAGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCCGAGGCTGGAGCCGAGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACGGAGGCCGAGGCTGAACGGCGAGAACCGCGAGATCCTG 159 1531 GACATCGTGCCCTGACCGAGAGGCCGAGAACCGCGAGAACCGCGAGATCCTG 159 1548 AIGGINLYSGINGINTYTYRASPPROAIALeuBroLeuArgAIaLysValleu 517	398 ThrTrpGlyPheLysThrProGluLysPheGlnLysAspProProTyrLeuTrpMet 417 1351 CCCATCGAGCTGCACCCGACAAGTGGACCGCATCGAGCTGCCCGAGAAGGAG 141. 418 GlyTyrGluLeuTyrProLysLysTrpGlnLeuGluGluIleThrLeuProGluArgGlu 437 1411 AGCTGGACCGTGAACATCCAGAGCTGGCGCAGCTGACCGAGATCTGGCCCGAGATCTGTGCACCCGAGATCTGTGCAGCCGAGAGCTGGCCAGAGCTGGCCAGAGCTGAGCAGCTGGCCAGCCA	398 ThrTrpGlyPheLysThrProGluLysPheGlnLysAspProProTyrLeuTrpMet 417 1351 CCCATCGAGCTGCACCCGACAAGTGGACCGCTCGAGCTGCCCGAGAAGGAG 141 418 GlyTytGluLeuTyrProLysLysTrpGlnLeuGluGluIleThrLeuProGluArgGlu 437 1411 AGCTGGAACGTGCAAGCTGGGCGCAAGCTGACCCGAGAAGTG 141 438 GluTrpThrValAsnaspIleGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIle 457 1471 TACCCGGCATCAAGGTGCGCAGCTGTGCAAGCTGCGCGCGC	398 ThrTrpGlyPheLysThrProGluLysPheGlnLysAspProProTyrLeuTrpMet 417 1351 CCCATCGAGCTGCACCCGACAAGTGGACCGCATCGAGCTGCCCGAGAAGGAG 1416 418 GlyTyrGluLeuTyrProLysLysTrpGlnLeuGluGluIleThrLeuProGluArgGlu 437 1411 AGCTGGACCGTGAACATCCAGAGCTGGCGAGACTGACTGA	1351 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GluTrpThrValAsnAsplleGlnLysLeuValGlyLysLeuAsnTrpalaSerGlnIle (15) 415 GluTrpThrValAsnAsplleGlnLysLeuValGluCatGAGCCGAGAACCGCAGATCCTG (15) 416 GluTrpThrValAshAsplleGlnTrpThrAsplaCatGAGCCGAGAACGCGAGATCCTG (15) 417 GACATGGTGCCCAGAGGAGCCCAGAGACCCCAGAAACGCGAGATCCTG (16) 418 ArgGlnLysGlnGlnGlyGlnTrpThrAspproAlaLeuProLeuArgAlaLysValLeu (17) 419 AGCAGGCCAGACCAGACGACCACCACACAAGACCCTACAAGAACCTGAAGATCCG (16) 410 GCGGAAGCCAGACGACCACCACACAAGACCCTACAAGAACCTGAAGATCCG (18) 410 GCGGAAGATGGCCAAGAACACCACACAAGAACCCCCAAGATCCG (18) 411 GCCGGAAGATGCAAGAACACCACCAAGAACCCCCAAGAACCCCCAAGATCCG (18) 411 GCCGGAAGATGCCAAGAACACCAACAAGAACCCCCAAGAACCCCCAAGATCCG (18) 412 GlyLysTyralaLysIleGlyLysGluSaTThrAshGluLeuArgMetLeuAlaGly (17) 413 GCGTGCAAAGAACCCAAGAACCTGGAACCCCCAAGAACCCCCAAGAACCCCCAAGAACCCCCAAGAACCCCCAAGAACCCCCAAGAACCCCCAAGAACCCCAAGAACCCCAAGAACCCCCAAGAACCCCAAGAACCCCAAGAACCCCCAAGAACCCCCAAGAACCCCAACCAAGAACCCCCAAGAACCCCAACCAAGAACCCCCAAGAACCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAAGAACCCCCAACCAACAA	1951 CCCATCGAGCTGCACCGACCAGGAGCCCATCGAGCTGCCCGAGAAGGA [141] 418 GlyTyTGLLLeuTyPErCyglysfireTagaCCGTGCAGCCCATCGAGCTGCCCGAGAAGGA [141] 418 GlyTyTGLLLeuTyPErCyglysfireTalacacGTGCCCAGCACGCCCAGCAGGAGGA [141] 418 GlyTyTGLLLeuTyPErCyglysfireTagaCCGTGCAGCCCAGCCCCAGCCCCAGCTCAGCCCCAGCTGAGCTGGAGCCAGCC	1951 CCCATCGACTGCACCCGACCAGGACCCATCGACGCGCGACAAGGAG 1410	1351 CCCATCCAGCTGCACCACACACTGCAGCCCACACCACAC	1351 CCCATCGAACTCCCACACACTGACCCCCACACACCCCACACACCCCACACACCCCACACACCCC	131 CCATCGAGCTGACCCCACAGAGGGCCGAGAGGGGC 131 CCATCGAGCTGACCCCCCCCACAGAGGGG 131 CCATCGAGCTGACCCCCCCCCCCCCCCCCCCCCCCCCCC	338	131 CCATGGACTACACCACACACACACACACACACACACACAC	131 CCATCGGGCTGGAGGGGCTGCGCGCAGGGGGCTGCGGGGGGGG	>	97 CGCTGGGGCTTCACCACCCCCGACAAGAACACCAGAAGGAGCCCCCCTTCCTG 13
1123 CAGGGCTGGAAGGCCCCAGCATCTTCCAGAGCAGCATGACCAGGATCCTGGAGCCC 11. 318 GlnGlyTrpLygGlySerProThrIlePheGlnThrThrAlaAsnLygIleLeuGlnGlu 35 1183 TTCCGGCCCGCAACCCGGGATCGTGATCTACCAGGCCCCCTGTACGAGGC 12. 1183 TTCCGGCCCGCAACCCGGGATCGTGATCTACCAGGCCCCCTGTACGTGGGC 12. 158 PheArgGlnLysAsnProAspValAspIleTyrGlnTyrMetAspAspMetLeuIleAla 37. 1237 AGCGACCTGGAGATCGGCGGCGAGATCGAGGAGCTGCGCAAGCACCTGCTG 12. 124 AGCGACCTGGAGATCGGCCGCGCCAGATCGAGAGCTGCGCAAGACCTGCTG 12. 125 AGCGACCTGGAGATCGGCCGCCGCCAGATCGAGAGCTGCCCTGCTG 13.	1351 CCCATCGAGCTGCACCGGACAGAGCGGCGGGCCCATCGAGCTGCCCGAGAAGGAG 14	1351 CCCATCGAGAGGAGCGGAGCGGGCCCATCGAGCTGCCCGAGAAGGAG	1351 CCCATCGAGCTGCACCCCGACAAGTGGACCGTCGAGCTGCCCGAGAAGGAG 141. 418 GlyTyrGluLeuTyrProLysLysTrpGlnLeuGlnGlulleThrLeuProGluArgGlu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCGAAAGCTGAACTGGGCCAGCCA	1351 CCCATCGAGAGGAGCCGAGCAGCCCATCGAGCTGCCCGAGAGGAG	1351 CCCATCGAGCTGCACCCGACAAGTGGACCGTCGAGCTGCCCGAGAAGGAG 141. 418 GlyTyrGluLeuTyrProLysLysTrpGlnLeuGlnGlulleThrLeuProGluArgGlu 437 1411 AGCTGGAACGTGAACGTCAGAAGCTGGTGGGCAAGCTGAACTGGCCAGCCA	1351 CCCATCGAGCTGCACCAGGAGCCCATCGAGCTGCCCGAAAGGAG 141.	1351 CCCATCGAGCTGCACCCGAGCAGCCCCATCGAGCTGCCCGAGAAGGAG 141	1351 CCCATCGAGCTGCACCAGGAGCCCATCGAGCTGCCCGAAAGGAG 141. 418 GlyfyrGluLeufyrFroLysfysfrpGluLeuGluGluLleffhrLeubroGluArgGlu 437 1411 AGCTGGAACCGTGAACGCTGCAGCTGGAGCTGACCGAGCTGATC 147. 1438 GluffyrhrValAsnaspileGluLysfueuValGlyLysfeuAsnTrpAlaSerGluI	1351 CCATCGAGCTGCACGACGAGCCGCCATCGAGCTGCCCGGAAAGGAG 141	1351 CCCATCGAGCTGCACCCGAGAAGGAG 141	1351 CCCATCGAGCTGCACCACGACGAGCCCATCGAGCTGCCCGAGAAGGAG 141. 418 GlyyrGluLeuTyrProLysLysTrpGlnLeuGlnGluIleThrLeuProGluArgGlu 437 1411 AGCTGGACCGTCAACGACACCTGGAGCGCAGCCGAGCCG	1351 CCCATCGAGCTGCACGACGAGCCCCATCGAGCTGCCCGAGAAGGAG 141	1351 CCCATCGAGCTGCACCAAGTGGACCGTGCAGCCCATCGAGCTGCAGAAGGAG 1418	1351 CCCATCGAGCTGCACCCGACAAGTGGACCCGACCGAGCAGAAGGG	1351 CCCATCGAGCTGCACCGGACAGGGCCCATCGAGCTGCCCGAGAAGGA 1418	1351 CCCATCGAGCAGCAGCAGAGCCCGAGCCCAGAGGGG 141 418 GlyTytdlubeutyErpolysistpolnieudinglulifnrieuricodlubrigdiu 437 418 GlyTytdlubeutyErpolysistpolnieudinglulifnrieuricodlubrigdiu 437 418 GlyTytdlubeutyErpolysistpolnieudinglulifnrieuricodlubrigdiu 437 418 GlyTytdlubeutyErpolysistpolnieudinglulifnrieuricodlubrigdiu 437 419 GlyTytdlubeutyErpolysistpolnieuricodlubrigdiu 437 410 TACCCGCACCACCACCACCACCACCACCACCCCCCCCCC	1351 CCCATCGAGCTGCACCACAAGTGGACCCCACACGAGGGG 141 418 GlyTytdlubeuVprProbyslystrpdlnieudinglulleThrieuprodlubrgglu 437 1411 AGCTGGACCGTGAACACACACACACACGCGCACACACCCACACACA	1351 CCCATCGAGCTGCACCGACAGTGGACCGCGCGCGCGCGCG	1351 CCATCGAGCTGGACCCCCCAGAAGACCCCATCGAGCTGCCCGAGAAGAGACCCATCGAGCTGGACCCCACCCA	1351 CCCATCCAGACCCACCACCAGAAGCCCCACCCAGAAGGA 14 14 14 14 14 14 14 1	1351 CCCATCGAGGAGCCCCCAAAGGACCTCGAGCCCCCCAAAGGGG 141 418 GIYTYGIULeuTyEProLygLyGTTyGInLeuGInGIUITeThrLeuProGluArgGIU 437 418 GIYTYGIULeuTyEProLygLyGTTyGINLeuGINGIUITeThrLeuProGluArgGIU 437 419 GIYTYGIULeuTyEProLygLyGTTyGINLeuGIUITeThrLeuProGluArgGIU 437 410 GIATTETHII	Ω	98 ThrirpGlyPheLysThrProGluLysLysPheGlnLysApproProTyrLeuTrpMet 41
1123 CAGGGCTGGAAGGCCCCAGCATCTTCCAGAGCATGACCAAGATCCTGGAGCCC 1113	418 GlyTyrdiuLeuTyrProLysLysTrpGlnLeuGinGluileThrLeuProGluArgGlu 43	418 GlytyrdluLeuTyrbroLyskystrpGlnLeudinGluileThrLeubroGluhrgGlu 437 1411 AGCTGGACCGTGAACGACACCGGGGGGGGGCAGCTGAACTGGGCCAGATC 1477	418 GlytyráluLeutyrProLygLygTrpGlnLeuGinGluileThrLeuProGluArgólu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCCAAGCTGAACTGGGCCAGCCA	418 GlytyrdluLeutyrPricystystrpGlnLeudinGluileThrLeuProdlubregdlu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAACTGGGCCAGCCA	418 GlyTyrdluLeuTyrProLygLygTrpGlnLeuGlnGluileThrleuProGluhrgGlu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCCAACTGACTG	418 GlytyrdluLeuTyrPricysLysTrpGlnLeuGinGluileThrLeuProGlubrgGlu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGGGCAACTGGGCCAGCCA	418 GlyTyrdiuLeuTyrPrictyglysTrgGlnLeuGinGluileThrLeuProGlubrgGlu 437 1411 AGCTGGACCGTGAACGACTCCAGAAGCTGGTGGCCAGCCA	418 GlytydiuLeutyrPricysivsTrpGlnLeudinGluileThrLeuProdiurggiu 437 1411 AGCTGGACCGTGAACGACAGCTGGGGGCAACTGGACCAGCCAG	418 GlyTyrdiuLeuTyrPricysLysLyslingluideudingluileThrieuProdiuzegdiu 437 1411 AGCTGGACCGTGAACGACTCGGTGGCGCAAGCTGGACCTGGACCAGCCAG	418 GlyfyrdiuLeufyrPricyglystrolnieudinGluileThrieuProdiurgdiu 437 1411 AGCTGGACCGTGACGACACCTGGGGCGCAAGCTGAACTGGCCCAGCCAG	418 GlyTyrdiuLeuTyrPricysLysLyslingluileUlidluileuProdiuArgdiu 437 1411 AGCTGGACCGTGAACGACTCGAGAGCTGGCCGAACTGGCCCAGCCAG	418 GlyTyrdiuLeuTyrPricysLysLyslingluideudinGluileThrieuProdiubrgdiu 437 1411 AGCTGGACCGTGAACGACTCGAGAGCTGGCGCAGCCAGCC	418 GlyTyrdiuLeuTyrPricLysLysTrginLeuGinGluileThrLeuPricliukrigiu 437 1411 AGCTGGACCGTGAACGACTCCAGAAGCTGGCGCAACTGGACCAGCCAG	418 GlyTyrśluieuTyrkolukeuTyrkolukeuGluieitierhrLeukroślukrgólu 437 1411 AGCTGGACCGTGAACGAACTGGAAGCTGGAAGCTGAACTGGACCGAGCCAGCTGATC 438 GluTrpThrValAmanApileGluLysteuValGlyLysLeuAmartzhalaSerGlille 457 1471 TACCCGGCATCAAGGTGCGCTGCTGCAAGCTGCGCGCGCCCCAAGGCCTGACC 153 1486 HyrThrGlylleLysThrJysHisLeuCySArgLeulieArgGlyAlaArgProLeuThr 477 1531 GACTGGTGCCCTGACCGAGGGGGGGGGCGGGCGGGCGCGAGGTCCTG 159 1531 GACTGGTGCCCTGACCGAGGGGGGGGGGGGGGGGGGGAACCCTG 159 1531 GACTGGTGCCCTGACCGAGGGGGGGGGGGGGGGGGGGGG	418 Glytyrdiuleutyrbrolysiyshrbolneudinglulientrieubrodiuargdiu 437 1411 AGCTGGACCGTGAACGACATCCAGAAGCTGGGCAACTGGCCCAGCCCAGATC 438 GlutrpThrVallanshplledinLysteuValdysteuNantrphlasserdinile 457 1471 TAGCTGCACCTGACGTGCCCAGCTGCTGGCGGGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCCAGACTGCCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTGCCCAGACTCCAGACTGCCCAGACTCCAGACTGCCCAGACTCCAGACTGCCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCAGACTCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCAGACTCCCAGACTCCCAGATCCCCAGATCCCCAGACTCCCAGATCCCCAGATCCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAGACTCCCAAGATCCCCAGACACCCCCAAGATCCCCAGACACCCCCAAGATCCCCAGACACCCCCAAGACCCCCAAGATCCCCAGACACCCCCAAGATCCCCAAGATCCCCAAGATCCCCAAGATCCCCAAGACCCCCAAGACACCCCCAAGATCCCCAAGATCCCCAAGACCCCCAAGACACCCCCAAGATCCCCAAGACACCCCCAAGATCCCCAAGATCCCCAAGATCCCCAAGATCCCCAAGACCCCCCAAGACACCCCCCAAGACACCCCCCAAGACACCCCCC	418 GlyTyrálujeuTyrProLysiystrpGlnLeuGinGluilerhrLeuPródlukrgálu 437 1411 AGCTGGACCGTGAACGACGAAGCTGGTGGCCAAGCTGAACTGGGCCAGACT 438 GluTrpThrValAsnAsplieGlnLysLeuValGlyLysLeuAsnTrpAlaSerGlnIle 457 1471 TACCCGGCATCAAGGTGCCCCACCTGGCAGCTGCTGGCGCGGCGCCAGACCTGACC 153 1471 TACCCGGCATCAAGGTGCCCCACCTGCAAGCTGCTGCGCGGCGCAGACCTGGTGCTGAGCTGGTGCTGAGCTGGTGAAGCTGGTGGCGCGGGGAACCCTGACC 153 1511 GACATCGTGCCCGTGACCGAGGAGGCGGAGCTGGTGGCGCGAGAACCGTGAGTGTGGTGGTGGTGTGTGT	411	111	111	18	118 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pleuGluH18AspArgValValLeuGlnLeuLysGluLeuLeuAsnSerLeuGlyPheSe
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pol polyprotein - human immunodeficiency virus type 2
pol polyprotein - human immunodeficiency virus type 2, HIV-2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: 853092
R;Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
8ubmitted to the EMBL Data Library, March 1995
A;Description: Molecular and phylogenetic characterisation of a Guinea-Bissau-de
A;Reference number: S53091
A;Reference number: S53091
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1055 < BEC>
A;Cross-references: UNIPROT:073194; EMBL:Z48731
C;Superfamily: pol polyprotein
C;Keywords: polyprotein
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                    GACAAGAGCGAGAGCGAGCTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAG 2250
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Pred. No.:
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J. Virol. 73:4427-4432(1999).
-!- SIMILARITY: Belongs to peptidase family A2.

EMBL. AF110975; AAD17135.1; -.
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GG) GG:001919; F:aspartic-type endopeptidase activity; IEA.

GG) GG:00034190; F:aspartic-type endopeptidase activity; IEA.

GG) GG:000351; F:DNA binding; IEA.

GG) GG:0008233; F:peptidase activity; IEA.

GG) GG:0004523; F:RNA binding; IEA.

GG) GG:0003723; F:RNA binding; IEA.

GG) GG:0003723; F:RNA directed DNA polymerase activity; IEA.

GG) GG:0001509; F:aranferase activity; IEA.

GG) GG:0001674; F:ranferase activity; IEA.
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Noviteky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
             06x4p0
08ade9
08ade3
08ada7
08adb7
08adb7
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Last sequence update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                    08AD29
08ADB9
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07SV30
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08ADN7
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09WLJ3
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Q9WF68
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  -MODEL=frame+ n2p.model -DEV=x1h
-WODEL=frame+ n2p.model -DEV=x1h
-Q=/cgnz 1/USFPTO epool/1905640313/runat 31052005 155136 15147/app_query.fasta 1.7893
-Q=/cgnz 1/USFPTO epool/1905640313/runat 31052005 155136 15147/app_query.fasta 1.7893
-DB=UniProt_03 -OFMT=fastan -SUFPIX=n2p.rup -MINNATCH=0.1 -LOOPCIL=0 -LOOPCIL=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TAINGN=15 -MODE=LOCAL
-OUTFWT=pto -NORM=ext -HEAFSIZE=560 -MINLEN=0 -MAXLEN=200000000
-USER=US09610313 @CGN 1 1.725 @runat 31052005 155136 15147 -NCPU=6 -ICPU=3
-NO WMAP -LARGEQUERY -NGG SCORES=0 -WAAT -DSPBEDCK=160 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6
                                                                               June 1, 2005, 20:20:55 ; Search time 208.158 Seconds (without alignments) 12088.668 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                         protein search, using frame_plus_n2p model
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R Pfam; PF00607; Gag_D24; 1.

R Pfam; PF00607; Raasel, 1.

R Pfam; PF00605; Rasel; 1.

R Pfam; PF0065; Rve; 1.

R Pfam; PF00065; Rve; 1.

R Pfam; PF00617; RVP; 1.

R Pfam; PF00615; RVT connect; 1.

R Pfam; PF0611; RVT chumb; 1.

R Pfam; Pfam; Pf0611; RVT chumb; 1.

R Pfam; Pfam; Pf0611; RVT chumb; 1.

R Pf0611; R
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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 Gag_p24.
Integrase_C.
Integrase_Zn_N.
Peptidase_A2.
Pept_Aspartic.
Pept_Aspartic.
Pept_Asp_AS.
Retrovir_matrix.
Retrovir_matrix.
Retrov_capsid_C.
Retrov_capsid_O.
Retrov_capsid_N.
                                                                                                                                                                                                             RVT connect.
RVT thumb.
Znf CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.67e-155
4097.00
98.98%
98.85%
89.95%
InterPro; IPR000721; GainterPro; IPR001037; In
InterPro; IPR001995; Pu
InterPro; IPR001995; Pe
InterPro; IPR001995; Pe
InterPro; IPR001999; Re
InterPro; IPR000071; Re
InterPro; IPR000916; Re
InterPro; IPR008916; Re
InterPro; IPR00199; Re
InterPro; IPR00199; Re
InterPro; IPR00156; Ru
InterPro; IPR00156; Ru
InterPro; IPR00156; Ru
InterPro; IPR00156; Ru
                                                                                                                                                                                                                                InterPro; IPR010661;
InterPro; IPR001878;
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Percent Similarity:
Best Local Similarity:
Ouery Match:
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Pred. No.:
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13 ATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGATGCAGCGCAGCAACTTC 72
                  Basex M.;
"Molecular cloning and phylogenetic analysis of human immunodeficiency
virus type 1 subtype C: a set of 23 full-length clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
                                                                                                                                                         Massy; Augusti, Churkinn, IEA.

GO; GO:0019190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0003190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0008233; F:DAB binding; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:000175; F:nthegrase activity; IEA.

GO; GO:000175; F:RNA binding; IEA.

GO; GO:000176; F:RNA-directed DNA polymerase activity; IEA.

GO; GO:000198; F:structural molecule activity; IEA.

GO; GO:000170; F:transferase activity; IEA.

GO; GO:000170; F:transferase activity; IEA.

GO; GO:00015074; P:DNA integration; IEA.

GO; GO:0006310; P:DNA integration; IEA.

GO; GO:0006310; P:NNA-dependent DNA replication; IEA.

GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
   Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1427 AA; 161293 MW; 270F25DF67615C06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                        Botswana.";
J. Virol. 73:4427-4432(1999).
-1- SIMILARITY: Belongs to peptidase family A2.
BEBL; AF110974; AAD17126.1; -.
HSSP; P04585; 1JLA.
                                                                                                                                                           GO; GO:0019012; Currion; IEA.
GO; GO:00019012; F:sapartic-type endopep
GO; GO:00019012; F:DRA binding; IEA.
GO; GO:0001807; F:DRA binding; IEA.
GO; GO:0001823; F:peptidase activity; I
GO; GO:0001823; F:peptidase activity; I
GO; GO:0001804; F:RNA-directed DNA poly;
GO; GO:0001807; F:RNA-directed DNA rep
GO; GO:0001807; F:RNA-directed DNA rep
GO; GO:0006208; P:Proteolysis and peptid
GO; GO:0006208; P:Proteolysis and peptid
GO; GO:0006208; P:Proteolysis and peptid
GO; GO:0006208; P:Protal life cycle; IEA
INTERPO; IPR000103; Integrase C.
INTERPO; IPR001995; Peptidase AZ.
INTERPO; IPR001995; Peptidase AZ.
INTERPO; IPR001995; Peptidase AZ.
INTERPO; IPR001995; Peptidase AZ.
INTERPO; IPR001995; Retrovir matrix.
INTERPO; IPR001991; Retrovir matrix.
INTERPO; IPR001991; Retrovir pl7.
INTERPO; IPR001991; Retrovir gold.
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PROSITE; PSO5175; ASP_PROT.
PROSITE; PSO5158; ZP CHC; ZP CHC; 1.
AIDS; Aspartyl protease; Core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000477; RVTse.
InterPro; IPR010659; RVT_connect
InterPro; IPR010661; RVT_thumb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00077; RVP; 1.
Pfam; PF00078; RVT 1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_chumb; 1.
Pfam; PF00098; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNPINGER.
PRINTS; PR00934; HIVIAMATRIX.
SWART; SM00343; ZnF_C2HC; 2.
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4093.00
98.85%
98.73%
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Integrase_Zi
RnaseH; 1.
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InterPro; IPR001584; Rve.
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Pfam; PF00607; Gag p24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR001878;
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Best Local Similarity:
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Pfam; PF00665; r
Pfam; PF00077; R
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG 2340
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                                                                                                                             LysLeuLeuArgGlyAlaLysAlaLeuThrAspIleValProLeuThrGluGluAlaGlu 879
                                                                                                                                                                                                       920 IleTyrGlnGluProPheLysAsnLeuLysThrGlyLysTyrAlaLysMetArgThrAla
                                                      940 HisThrAsnAspValLysGlnLeuThrGluAlaValGlnLysIleAlaMetGluSerIle
                                                                                                                                                                                                                                                                                                                                                   960 ValileTrpGlyLysThrProLysPheArgLeuProlleGlnLysGluThrTrpGluThr
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                                  CTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCCGTGCACGGCGTGTACTACGAC
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MEDLINE-99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
vi.1
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                                                                                                                                                                                                                                                                                                               Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 LeuAlaGluAlaMetSerGlnAlaThrSerAlaAsnIleLeuMetGlnArgSerAsnPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheProGlnIleThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlyGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AACTGCCGCCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGCCCACCAGATG
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R Pfam; PF00065; rve; 1.

R Pfam; PF00077; RVP; 1.

R Pfam; PF06815; RVT_connect; 1.

R Pfam; PF06817; RVT_connect; 1.

R Pfam; PF06817; RVT_connect; 1.

R Pfam; PF06817; RVT_connect; 1.

R RFINTS; PR00939; ZCHCZNFINGER.

R RRINTS; RR00343; ZLP CZHC; 2.

R RRINTS; RR00143; ZP CZHC; 2.

R RROSITE; PS00141; ASP PROTEASE; 1.

R RROSITE; PS50175; ASP PROT RETROV; 1.

R RROSITE; PS50175; ASP PROT RETROV; 1.

R ROSITE; PS50175; ASP CHOT RETROV; 1.

R RIDS; ASPATY1 Drotease; RNA-directed DNA polymerase; Transferase; Zinc
                                                                                                                                                                                                                                                                                                                                                           1428 AA; 161328 MW; 2D61CD9FEABD2387 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
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98.60%
89.77%
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Best Local Similarity:
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                          Essex M.; "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from
                                                                                                                     GGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virus Type 1 subtype C: a set of 23 full-length clones from botswara.";

J. Virol. 73:4427-4432(1999).

G. Virol. 73:4427-4432(1999).

EMBL; ARILORYT'S Belongs to peptidase family A2.

EMBL; ARILORYT'S Belongs to peptidase family A2.

EMBL; ARILORYT'S Belongs to peptidase activity; IEA.

GO; GO:00019012; C: virion; IEA.

GO; GO:0003677; F:lontegrase activity; IEA.

GO; GO:0003723; F:RNA-binding; IEA.

GO; GO:0003723; F:RNA-binding; IEA.

GO; GO:000374; F:lontegrase activity; IEA.

GO; GO:0006719; F:ransferase activity; IEA.

GO; GO:0006710; F:ransferase a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
                                                                                                                                                                                                                                                                                                                                                                                             Ol-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NNV-1999 (TrEMBLrel. 26, Last annotation update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000477; RVTse.
InterPro; IPR010659; RVT_connect.
InterPro; IPR010661; RVT_humb.
InterPro; IPR01188; Znf_CCHC.
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PF00607; Gag_p24; 1.
PF02022; Integrase_Zn; 1.
PF00075; RnaseH; 1.
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                       GTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGGACCTGGGAAGCA
                                               TrpTrpThrAspTyrTrpGlnAlaThrTrp1leProGluTrpGluPheValAsnThrPro
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MEDLINE=99214383; PubMed=10196340;

MEDLINE=99214383; PubMed=10196340;

A Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

A Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,

Essex M.;

"Molecular cloning and phylogenetic analysis of human immunodeficit

"virus type 1 subtype C: a set of 23 full-length clones from

Botswana."

J. Virol. 73:4427-4432(1999).

C -! - SIMILARITY: Belongs to peptidase family A2.

EMBL; AF110961; AAD17021.1; -.

R GSS; QC:0019012; C:virion; IEA.

GO: QC:0014910; F:aspartic-type_endopeptidase activity; IEA.
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GO:0004190; F:aspartic-type endopeptidase activity; IEA.
GO:0004190; F:negratic-type endopeptidase activity; IEA.
GO:0008907; F:integrase activity; IEA.
GO:000833; F:peptidase activity; IEA.
GO:0004523; F:ribonuclease H activity; IEA.
GO:0003723; F:RNA binding; IEA.
GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
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01-NOV-1999 (TERBLIE1.12, Created)
01-NOV-1999 (TERBLIE1.12, Last sequence update)
01-MAR-2004 (TERBLIE1.26, Last annotation update)
6ag-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                       TTGGCCATCAAGAAGAAGACAGCACCAAGTGGGGGCAAGCTGGTGGACTTCCGCGAGCTG
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                                             GTGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAG
                                                                                                                                       ATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCGTG
                                                                                                                                                                 640 PheAlaIleLysLysLysAspSerThrLysTrpArgLysLeuValAspPheArgGluLeu
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TyrGlnTyrMetAspAspLeuTyrValGlySerAspLeuGluIleGlyGlnHisArgAla 779
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       LysAlaArgGluPheProSerGluGlnThrArgAlaIleSerProThrSerArgGluLeu
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                                                AsnLysArgThrGlnAspPheTrpGluValGlnLeuGlyIleProHisProAlaGlyLeu
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                                                                                        373 TICCCCCAGAICACCCTGTGGCAGCGCCCCTGGTGAGCAICAAGGTGGGCGGCCAGATC
                                                                                                                                             AAGGAGCCCTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCC
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PRINTS; PRO0334; HIVIMATRIX.
SMART; SM00343; C2HCZNCIX.
PROSITE; PS00141; ASP_PROTEASE; 1.
PROSITE; PS50175; ASP_PROT_RETROV; 1.
PROSITE; PS50175; ASP_CGHC, 2.
AIDS; Asparty1 protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase;
GO; GO:0005188; F:structural molecule activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008270; F:zinc lon binding; IEA.
GO; GO:0006210; F:zinc lon binding; IEA.
GO; GO:0006310; P:DNA integration; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006312; P:WA-dependent DNA replication; IEA.
GO; GO:000632; P:WA-dependent DNA replication; IEA.
GO; GO:001632; P:WA-dependent DNA replication; IEA.
R InterPro; IPR001037; Integrase_Zn.
R InterPro; IPR001037; Integrase_Zn.
R InterPro; IPR001995; Peptidase_A2.
R InterPro; IPR001995; Peptidase_A2.
R InterPro; IPR001999; Retrovir_matrix.
R InterPro; IPR001999; Retrovir_matrix.
R InterPro; IPR001916; Retrovic_apsid_C.
R InterPro; IPR001916; Retrovic_apsid_N.
R InterPro; IPR001916; Retrovic_apsid_N.
R InterPro; IPR001916; Retrovic_apsid_N.
R InterPro; IPR001916; Retrovic_apsid_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1427 AA; 160992 MW; AC2ACBF190C77DAD CRC64
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                 RVTse.
RVT_connect.
RVT_thumb.
Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF00540; Gag_D17; I. Pfam; PF00202; Integrase_Zn; I. Pfam; PF00202; Integrase_Zn; I. Pfam; PF00075; RnaseH; I. Pfam; PF00077; RVP; I. Pfam; PF00077; RVP; I. Pfam; PF06815; RVT_Linat; Pfam; PF06815; RVT_Connect; I. Pfam; PF06817; RVT_Connect; I. Pfam; PF06817; RVT_Connect; I. Pfam; PF00691; zf-CCHC; 2.
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3947.00
96.82%
94.40%
86.65%
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Interpro; IPR001999; Re
Interpro; IPR008916; Re
Interpro; IPR008916; Re
Interpro; IPR008919; Re
Interpro; IPR001919; Ri
Interpro; IPR001584; RV
Interpro; IPR001684; RV
Interpro; IPR010669; RV
Interpro; IPR010669; RV
Interpro; IPR010661; RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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PubMed=14709249; DOI=10.1089/088922203771881220;
PubMed=14709249; DOI=10.1089/088922203771881220;
Harris M.E., Maayan S., Kim B., Zeira M., Ferrari G., Birx D.L.,
McCutchan F.E.;
M. Culster of HIV type 1 subtype C sequences from Ethiopia, observed in full genome analysis, is not sustained in subgenomic regions.";
AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hadyan S., Zeira M.;

Maayan S., Zeira M.;

Maayan S., Zeira M.;

Maayan S., Zeira M.;

Maayan S., Zeira M.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY Belongs to peptidase family A2.

EMBL; AV25S825; AAP76538.1; ---

EMBL; AV25S825; AAP76538.1; ---

EMBL; AV25S825; AAP76538.1; ---

EMBL; AV25S825; AAP76538.1; ---

CO; GO:0001902; E: Substitute-type endopeptidase activity; IEA.

GO; GO:0001902; F: Integrase activity; IEA.

GO; GO:0008207; F: Integrase activity; IEA.

GO; GO:0008207; F: Integrase activity; IEA.

GO; GO:0008207; F: F: EMA binding; IEA.

GO; GO:0008207; F: F: EMA binding; IEA.

GO; GO:0008207; F: Read binding; IEA.

GO; GO:0008207; F: Read binding; IEA.

GO; GO:0008207; F: Read binding; IEA.

GO; GO:0008207; F: P: EMA binding; IEA.

GO; GO:0008207; F: P: EMA binding; IEA.

GO; GO:0008207; F: P: EMA binding; IEA.

GO; GO:0008207; F: Read binding; IEA.

GO; GO:0008207; F: P: EMA directed DNA replication; IEA.

GO; GO:0008207; F: P: EMA-dependent DNA replication; IEA.

GO; GO:0008207; F: P: EMA-dependent DNA replication; IEA.

GO; GO:0008207; F: P: EMA-dependent DNA replication; IEA.

InterPro; IPR001037; Integrase C.

InterPro; IPR001099; Retrovely ABpartic.

InterPro; IPR001999; Retrovely ABpartic.

InterPro; IPR001999; Retrovely ABpartic.

InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterPro; IPR001999; Retrovely EMB InterP
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Harris M.E., Birx D.L.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim B., McCutchan F.E.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol fusion polyprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR010661; RVT_thumb.
InterPro; IPR001878; Znf_CCHC.
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Pfam; PF00078; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00098; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
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Integrase_Z
RnaseH; 1.
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Pfam; PF00607; Gag_p24
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=11676;
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SMART; SM00343; ZAP C2HC, 2.
PROSITE; PS00141; ZAP PROTEASE; 1.
PROSITE; PS00154; ASP PROTEASE; 1.
PROSITE; PS50154; ASP CCHC, 2.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Polyprotein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Salor-finger.

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	1489 858	CGCCAGCTGTGCAAGCTGCTGCGGGGCGCAAGGCCCTGACCGACC
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Bubmed-14709249; DOI=10.1089/088922203771881220;
Harris M.E., Maayan S., Kim B., Zeira M., Ferrari G., Birx D.L.,
McCutchan F.E.,
A cluster of HIV type 1 subtype C sequences from Ethiopia, observe
in full genome analysis, is not sustained in subgenomic regions.";
AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to peptidase family A2.
-- SIMILARITY: BAP76529.1;
-- HSSP; Q72498; 1K6Y.
G0; G0:0019012; C:virion; IEA.
G0; G0:0004190; F:appartic-type endopeptidase activity; IEA.
G0; G0:00004190; F:integrase activity; IEA.
G0; G0:0000807; F:integrase activity; IEA.
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Harris M.E., Birx D.L.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Kim B., McCutchan F.E.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol fusion polyprotein (Fragment).
Human immunodeficiency virus 1.
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NCBI_TaxID=11676,
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004523; F:ribonuclease H activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0005198; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0005270; F:Zinc ion binding; IEA.
GO; GO:0005270; F:Zinc ion binding; IEA.
GO; GO:0005270; F:Zinc ion binding; IEA.
GO; GO:0006270; F:RNA-dependent DNA replication; IEA.
InterPro; IPR001930; Pepti-Asp.As.
InterPro; IPR001949; Retrovir_matrix.
InterPro; IPR001959; Retrovir_matrix.
InterPro; IPR001954; Rva-
InterPro; IPR001954; Rva-
InterPro; IPR001954; Rva-
InterPro; IPR001965; Rva-
InterPro; IPR001966; Rva-
InterPro; IPR001967; Rva-
InterPro; IPR001966; Rva-
InterPro; I
                                                                                                                                   IEA.
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
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PROSITE; PSG0141; ASP_PROTEASE; 1.
PROSITE; PSG0175; ASP_PROT_RETROV; 1.
PROSITE; PSG0158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fram; PF00665; rve; 1.
Pram; PF00077; RVP; 1.
Pram; PF00078; RVT 1; 1.
Pram; PF06815; RVT _connect; 1.
Pram; PF06815; RVT _connect; 1.
Pram; PF06817; RVT _chumb; 1.
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Pfam; PF00607; Gag_D24; I.
Pfam; PF02022; Integrase_Zn; I.
Pfam; PF00075; RnaseH; I.
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PRINTS; PR00234; HIV1MATRIX.
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                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99214383; PubMed=10196340;
Noviteky V.A., Montano M.A., McLane M.E., Renjifo B., Vannberg F., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
"Molecular cloning and phylogenetic analysis of human immunodeficiency virus type I subtype C: a set of 23 full-length clones from
                                                                                                                                                                                                                                                                                                                                                                                      R GO; GO:0019012; C:virion; IEA.

GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.

GO; GO:0003677; F:DNA binding; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0003964; F:RNA binding; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:001679; F:structural molecule activity; IEA.

R GO; GO:001670; F:sinc ion binding; IEA.

R GO; GO:0006210; P:DNA integration; IEA.

R GO; GO:0006210; P:DNA integration; IEA.

R GO; GO:0006218; P:Porteolysis and peptidolysis; IEA.

R GO; GO:0006278; P:Porteolysis and peptidolysis; IEA.

R GO; GO:0010529; P:viral life cycle; IEA.
                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
63g-pol polyprotein.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                Botswana.";
J. Virol. 73:4427-4432(1999).
-!- SINLARITY: Belongs to peptidase family A2.
EMBL; AF110976; AAD17144.1; -.
HSSP; Q70622; 1HVN.
                                            PRT; 1427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0003577; F: DNA binding; IERO-
GO; GO: 0008307; F: Integrase activity; I.
GO; GO: 0008233; F: Pintegrase activity; I.
GO; GO: 0008233; F: Pintegrase activity; I.
GO; GO: 0008292; F: RNA binding; IEA-
GO; GO: 0003296; F: RNA binding; IEA-
GO; GO: 0008296; F: RNA binding; IEA-
GO; GO: 0008209; F: RNA binding; IEA-
GO; GO: 0008209; F: RNA binding; IEA-
GO; GO: 0008209; F: RNA combination; IEA-
GO; GO: 0006210; F: PNA recombination; IEA-
GO; GO: 0006209; P: PNA recombination; IEA-
GO; GO: 0006209; P: PNA recombination; IEA-
GO; GO: 0006209; P: PNA recombination; IEA-
INCETPO; IPR001037; Integrase CIN-
INCETPO; IPR001037; Integrase CIN-
INCETPO; IPR001995; Peptidase AS-
INCETPO; IPR001995; Peptidase AS-
INCETPO; IPR001995; Peptidase AS-
INCETPO; IPR001999; Retrovir_matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00343; ZNF C2HC; 2.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZP_CCHC; 2.
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InterPro; IPR010659; RVT connect.
InterPro; IPR010661; RVT_thumb.
InterPro; IPR010818; Znf_CCHC.
Pfam; PF00540; Gag_D17; I.
Pfam; PF00067; Gag_D24; 1.
Pfam; PF00022; Integrase Zn; 1.
Pfam; PF00075; RnaseH; 1.
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PF00077; RVP; 1.
PF00078; RVT; 1.
PF06815; RVT connect; 1.
PF06817; RVT chumb; 1.
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PRINTS; PR00234; HIV1MATRIX.
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                                            PRELIMINARY;
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Pfam;
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AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
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                                        1427 AA; 160518 MW; FBDA73D603A68B18 CRC64;
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726
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Matches:
Conservative:
Mismatches:
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                                                                             1.56e-147
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Best Local Similarity:
Query Match:
DB:
                                                                  Alignment Scores:
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                                        SEQUENCE
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1079 2220 1099 2280 11119 2340 1139

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1020 TyrValAspGlyAlaAlaAsnArgGluThrLysLeuGlyLysAlaGlyTyrValThrAsp
                                                                   1080 TyrAlaLeuGlyIleIleGlnAlaGlnProAspLysSerGluSerGluLeuValAsnGln
                                                                                                                                                                                                 GGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGCAAGGCAAGGTGCTG
                                                      CGGGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAGAAGACCGAGCTGCAG
                                                                                                 GCCATCCAGCTGGCCCTGCAGGACAGCGGCAGGGGGAGCTGAACATCGTGACCGACAGCCAG
                                                                                                                                           SECUENCE FROM N.A.

Pubmed=14709249; DOI=10.1089/088922203771881220;

Pubmed=14709249; DOI=10.1089/088922203771881220;

McCutchan F.E.;

Actuater of HIV type 1 subtype C sequences from Ethiopia, observe in full genome analysis, is not sustained in subgenomic regions."; AIDS Res. Hum. Retroviruses 19:1125-1133(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G0:0019912; C:virion; IEA.
G0:0004190; F:aspartic-type endopeptidase activity; IEA.
G0:0003677; F:DNA binding; IEA.
G0:0008237; F:integrase activity; IEA.
G0:0008233; F:peptidase activity; IEA.
G0:0004523; F:ribonuclease H activity; IEA.
G0:0003723; F:RNA binding; IEA.
G0:0003764; F:RNA directed DNA polymerase activity; IEA.
G0:0005198; F:structural molecule activity; IEA.
G0:0005198; F:structural molecule activity; IEA.
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Gag-pol fusion polyprotein (Fragment).
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Submitted (MAR-2003) to the
-!- SIMILARITY: Belongs to F
EMBL; AY255823; AAP76521.1;
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Submitted (MAR-2003) to
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Kim B., McCutchan F.E.;
Submitted (MAR-2003) to
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                                                                                                          GACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCCCAGCATCAACAACGAGACCCCC 1092
                                                                                                                                                    GGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCAGCATCTTC 1152
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Wholecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Strange virus type 1 subtype C: a set of 23 full-length clones from Grewara.

The Cores of Co
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PROSITE; PS50175; ASP_PROT_RETROV; 1.
PROSITE; PS50158; ZF CCHC; 2.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=9214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg I Novitsky V.B., Montano M.A., McLane M.F., Rahman M., Makhema M.J., Marlink R., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                  Gag-pol polyprotein.

Human immunodeficiency virus 1.

Viruses; Retroid viruses; Retroviridae; Lentivirus

Noll_TaxID=11676;
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InterPro; IPR00308; Integrase_Zn_N.
InterPro; IPR00308; Peptidase_A2.
InterPro; IPR009007; Pept_Aspartic.
InterPro; IPR01099; Retrovir_matrix.
InterPro; IPR000919; Retrovir_matrix.
InterPro; IPR008916; Retrovir_matrix.
InterPro; IPR008916; Retrov capsid_N.
InterPro; IPR008919; Retrov_capsid_N.
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InterPro; IPR010661; RVT_thumb.
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Pfam; PF00665; TvVe; 1.
Pfam; PF00077; RVP; 1.
Pfam; PF00615; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_chumb; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCHC.
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Integrase_Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001584; Rve
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Pfam; PF02022;
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Alignment Scores:

PRT; 1427 AA

Q9WF71; 01-NOV-1999 (TrEMBLrel. 12, Created)

PRELIMINARY;

Q9WF71

973 AAGAAGAAGAAGAGCGTGACCGTGGACGTGGGCCACGCCTTCAGCGTGCCCCTG 103:	1153 CAGAGCAGGATGACCAAGATCCTGGAGCCCTTCCGGCCCCCCCAACCCCGAGATCGTGATC 1212	AAGATCGAGGAGCTGCGCAAGCACCTGCGCTGGGGCCTTCACCACCCCCGACAAGAAG 132 [1381 GTGCAGCCCATCGACCGACAGGAGGAGCTGGACCGTGAACCATCCAGAGCTG 1440 :	1501 AAGCTGCTGCGCGCGCCAAGGCCCTGACCGACTGCTGCCCTGACCGAGGAGGCCGAG 1560	1621 CCCAGCAAGGACCTGGTGGCCGAGATCCAGAAGCAGGCCACGACCAGGACCAACCA	1741 CACACCAACGACGGGACCCGGGCCGTGCCAGAGATCGCCATGGAGAGCATC 1800	regreaccactregcaeccaccreagarcccaagagagarccgraaAcacccc 19	1981 TACGTGGACGCGCCAACCGGGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGGC 2040
8 6 6 6 6	% qa % qa	\$ 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	\$ G & G	\$ 6 & 6	& 92 & 93 84 & 94	6 6 6 6	\$ B \$
27 22	73 AAGGCCCCAAGCGATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCGC 13 73 AAGGCCCCCAAGCGATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCGC 13 80 LysGlyProArgArg11eValLysCysPheAsnCysGlyLysGluGlyHis1leAlaArg 39 133 AACTGCCGCCCCCGCAAGAAGGCTGCTGCAAGGAGGGCCACCAGATG 19	193 AAGGACTGCACCGAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCC 193 AAGGACTGCACCGCCAGGCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCC 194 AAGGACTGCACGCCAGGCCAACTTCTTCTCGCGAGGACCTGGCCTTCCCCC 195 AAGGACTTCCCAGGGCAACCGGCCCAACAGCCCCACAGCGCGCCCCCACAGCGGCG	Qy 313 CAGGGGGGACAACCCCGGAGGGGGGGCGCGGGGGCACCCTGAAC 372 Db	433 AAGGAGCCCTGCTGGACGCGCGCGACGACGTGCTGGAGGAGATGAGCCTGCCC 49 500 ArgGlualaLeuLeuAspThrGlyAlaAspAspThrValLeuGluAspIleAsnLeuPro 51 493 GGCAAGTGGAAGCCCAAGATGGCGGCGATCGCGGCTTCATCAAGGTGCGCGAGTAC 55	553 GACCAGATCCTGATCGAGGCAAGAAGGCCATCGGCACCGTGCTGATAGGTTAGGTTAGGTTAGGTTAGGTGATCGGCCCC 61 551 GACCAGATCCTGATCGAGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCC 61 552 GACCACTGATCGATCGGCAGCAGCAAGAAGGTGATGATTAGGTTAGGTGACCCAGCTGCACCTGAACTTC 67 613 ACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAGCTGCACCCTGAACTTC 67	snPhe 57 CCAAG 73 roLys 59 AGGAG 79	600 ValiysGlnTrpProLeuThrGluGluIysIleLysAlaLeuThrAlaIleCysGluGlu 61 793 ATGGAGAAGGAGGCAAGATCACCAAGATCGGCCCGAGAACCCCTACAACACCCCCGTG 85	DD 640 PREAIBALIELYBLYBLYBLYBLYBLYBLYBLEGUVALASPPREAIGIULEU 659 QY 913 AACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGGATCCCCCACCCGGCGGGCTG 972

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PheProGlnIleThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlnVal 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 AAGGCCCGCGAGTTCCCCAGCGAGCAGAACCGCGCCAACAGCCCCACCAGCCGCGAGCTG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 CAGGTGCGCGGCGACAACCCCCGCAGCGAGGCCGGCGCGAGGCCCAGGGCACCCTGAAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATC 432
                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0339; CZHCKNFINGER.
PRINTS; PRO0339; ZAPCZHCKNFINGER.
SMART; SM00343; ZAPCZHCZ, Z.
PROSITE; PRO0141; ASP PROTEASE; 1.
PROSITE; PSS0175; ASP PROTEASE; 1.
PROSITE; PSS0175; ASP PROT RETROV; 1.
PROSITE; PSS0175; Drotease; Corr protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 AAGGACTGCACCGAGCGCCAGCCCAACTTCTTCCGCGAGGACCTGGCCTTCCCCCCCAGGGC
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723
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Matches:
Conservative:
Mismatches:
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        Retrov capsid N.
                                                                                 InterPro; IPR010659; RVT_connect.
InterPro; IPR010661; RVT_thumb.
InterPro; IPR001861; Znf_CCHC.
Pfam; PF00540; Gag_D17; I.
Pfam; PP00607; Gag_D24; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF02025; RnaseH; 1.
                                                                                                                                                                                                                                                              Pfam; PF00078; RVT_1; 1.
Pfam; PF06815; RVT_connect; 1.
Pfam; PF06817; RVT_thumb; 1.
Pfam; PF00098; zf-CCHC; 2.
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3888.00
96.44%
91.98%
85.36%
                                                                  RVTse.
                           IPR002156; RNas. IPR001584; Rve.
                                                                                                                                                                                                                             rve; 1
RVP; 1
                                                            IPR000477;
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Best Local Similarity:
                                                                                                                                                                                                    Pfam; PF00075; R
Pfam; PF00665; r
Pfam; PF00077; R
Pfam; PF00078; R
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                         InterPro; I
InterPro; I
InterPro;
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DB:
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1080 TyralaLeuGly1leIleGlnAlaGlnProAspLy8SerGluSerGluLeuValThrGln 1099
                                                                                                                                                                                                                                               GGCATCGGCGCAACGAGCAGATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG 2340
                                                                                                                                                                                                                                                                                                                        1120 GlylleGlyGlyAsnGluGlnValAspLysLeuValSerSerGlylleArgLysValLeu 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from Botswana.";
                                                            GCCATCCAGCTGGCCCTGCAGGACAGCGGCGAGGTGAACATCGTGACCGACAGCCAG
                                                                                                                                                                                                                         MEDLINE=99214383; PubMed=10196340;
Noviteky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Besex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  December 1 13:4427-4432(1999).

C -!- SIMILABITY: Belongs to peptidase family A2.

R EMBL, A7110978; AAD17162.1; -..

PIR; 849086; 849086.

R 60; 60:0019012; C:virion; IEA.

R 60; 60:00019012; C:virion; IEA.

R 60; 60:00019012; F:integrase activity; IEA.

R 60; 60:0001807; F:integration; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Gag-pol polyprotein:
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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GO; GO:001912; F:sapartic-type endopep;
GO; GO:000167; F:sapartic-type endopep;
GO; GO:000167; F:DNA binding; IEA.
GO; GO:000823; F:peptidase activity; II
GO; GO:000823; F:peptidase activity; II
GO; GO:000172; F:NAA binding; IEA.
GO; GO:000172; F:NAA binding; IEA.
GO; GO:000180; F:transferase activity;
GO; GO:0006270; F:NAA integration; IEA.
GO; GO:0006270; P:NAA integration; IEA.
GO; GO:0006270; P:NAA dependent DNA rep)
GO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                      1040
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TACCAG------GCCCCCCTGTACGTGGGCACCTGGAGATCGGCCAGCACCAGCGCC 1266
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              400 AsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLysGluGlyHisGlnMet 419
                                                                                                                                                         PheAlalleLysLysAspSerThrLysTrpArgLysLeuValAspPheArgGluLeu 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 PheProGlnIleThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlyGlnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 ProlleSerProlleGluThrValProValLysLeuLysProGlyMetAspGlyProLys
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                                                                                                                                                                                                                    CAGGTGCGCGCGACAACCCCCCCGCAGGCCGGCGGCCGAGCGCCAGGCCACCCTGAAC
                                                                                                                                                                                                                                                                                                   TTCCCCCAGATCACCCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                         GGCAAGTGGAAGCCCAAGATGATCGCCGCCATCGGCGGCTTCATCAAGGTGCGCCAGTAC
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R EMBL; AP110962; AAD17030.1; ---
R HSSP; Q70622; LHVN.
GO; GO:0001912; C:virion; IEA.
GO; GO:0001902; C:virion; IEA.
GO; GO:0001903; F:aspartic-type endopeptidase activity; IEA.
GO; GO:0003677; F:INTA Dinding; IEA.
GO; GO:0003677; F:INTA Dinding; IEA.
GO; GO:0001904; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:0001905; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:00019064; F:RNA-directed DNA polymerase activity; IEA.
GO; GO:00010670; F:Zinc ion binding; IEA.
GO; GO:00018070; F:Zinc ion binding; IEA.
GO; GO:0006210; P:DNA integration; IEA.
GO; GO:0006210; P:DNA integrated.
GO; GO:00062010; P:DNA-directed DNA replication; IEA.
R InterPro; IPR001909; Pept-Aspartic.
R InterPro; IPR001999; Retrovir_matrix.
R InterPro; IPR0019166; RNA-depsid_C.
R InterPro; IPR0019166; RNA-depsid_C.
R InterPro; IPR0019166; RNA-depsid_C.
R InterPro; IPR0019166; RNA-depsid_C.
R InterPro; IPR001916; Retrov-capsid_C.
R InterPro; IPR001916; Rutov-capsid_C.
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SWART; SM00343; ZnF C2HC; 2.
PROSITE; PS00141; ASP PROTEASE; 1.
PROSITE; PS50175; ASP PROT RETROV; 1.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVT_connect.
RVT_thumb.
Znf_CCHC.
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InterPro; IPR001878;
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"Modecular cloning and phylogenetic analysis of human immunodeficiency virus type I subtype C: a set of 23 full-length clones from Botswana.",

J. Virol. 73:4427-4432 (1999).

-! SIMILARITY: Belongs to peptidase family A2.

EMBL, AFI10967, AAD17072.1; -.

HSSP; P24736; INCP.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F., Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R., Essex M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Histip 124/136; INCP.

RGO; GO: 00014910; E: aspartic-type endopeptidase activity; IEA.

RGO; GO: 0001490; F: aspartic-type endopeptidase activity; IEA.

RGO; GO: 0000823; F: DNA binding; IEA.

RGO; GO: 0000823; F: peptidase activity; IEA.

RGO; GO: 0000823; F: peptidase activity; IEA.

RGO; GO: 0000423; F: peptidase activity; IEA.

RGO; GO: 00013964; F: RNA-directed DNA polymerase activity; IEA.

RGO; GO: 00013964; F: RNA-directed DNA polymerase activity; IEA.

RGO; GO: 00015073; F: RNA-directed DNA polymerase activity; IEA.

RGO; GO: 00015074; F: princ ion binding; IEA.

RGO; GO: 00015076; F: princ ion binding; IEA.

RGO; GO: 0006270; P: princ ion binding; IEA.

RICEPPO; IPRO01999; Retrovir_matrix.

RICEPPO; REPOSONO1; Retrovir_matrix.

                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                           Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                           PRT; 1437 AA
                 Pfam; PP00078; RVT_1; 1.
Pfam; PP06815; RVT_connect; 1.
Pfam; PP06817; RVT_chumb; 1.
Pfam; PP00098; zf-CCHC; 2.
PRINTS; PR00039; C3HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_CZHC; 2.
                                                                                                                                                                                                                                  Gag-pol polyprotein.
Human immunodeficiency virus 1.
                                                                                                                           PRELIMINARY;
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Pfam; PF00077; RVP; 1
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PROSITE; PS50175; ASP_PROT RETROV; 1.
PROSITE; PS50175; ASP_PROT RETROV; 1.
AIDS; Aspartyl protease; Core protein; Hydrolase; Metal-binding; Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc-finger.
SEQUENCE 1437 AA; 161978 MW; 65DAA2562FC317A6 CRC64;
                                            1437
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                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                              US-09-610-313B-32 (1-2457) x Q9WF77
                                            1.06e-146
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Pred. No.:
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Best Local Similarity:
Query Match:
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GCGGGGCAGAAGATCGCCATGGAGGCATCGTGATCTGGGGCAAGACCCCCCAAGTTCCGC GlyTyrGluLeuHi8ProAspLysTrpThrValGlnProIleGlnLeuHroAspLysAsp AAGCAGGCCACGACCAGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAG ACCGGCAAGTACGCCAAGATGCGCACCGCCCAACCAACGACGTGAAGCAGCTGACCGAG ThrGlyLysTyrAlaLysMetArgThrAlaHisThrAsnAspyalLysGlnLeuThrGlu TGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAAGGACTTCTGGGAGGTG TrpArgLysLeuValAspPheArgGluLeuAsnLysArgThrGlnAspPheTrpGluVal Gragacacaccracricaacaraccccragacaacaacaracacaagracacacric CCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAG GACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTG CGCGAGCCCGTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTGGCCGAGATCCAG •

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CAGGTGCGCGGCGACAACCCCCGCGAGCCGGCGCGCGAGCGCCCAGGGCACCTGAAC 372
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REAL Wholecular cloning and phylogenetic analysis of human immunodeficiency virus type 1 subtype C: a set of 23 full-length clones from BCE Wanda. 13:4427-4432(1999).

C. 1- SIMILARITY: Belongs to peptidase family A2.

EMBL, ARI10956; AAD17056.1; -.

EMBL, ARI10956; AAD17056.1; -.

EMBL, ARI10956; AAD17056.1; -.

EMBC, AG0066; S49086.

CG G0:000419012; Civition; IEA.

GG; G0:000419012; Civition; IEA.

GG; G0:000419012; Fishpartic-type endopeptidase activity; IEA.

GG; G0:0004307; Fintegrase activity; IEA.

GG; G0:0004323; Fishpurdase activity; IEA.

GG; G0:0004323; Fishpurdase activity; IEA.

GG; G0:0005139; Fishructural molecule activity; IEA.

GG; G0:0005139; Fishructural molecule activity; IEA.

GG; G0:0005140; Fishructural molecule activity; IEA.

GG; G0:0005140; Fishructural molecule activity; IEA.

GG; G0:0005199; Fishructural molecule activity; IEA.
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           1000 IleProGluTrpGluPheValAsnThrProProLeuValLysLeuTrpTyrGlnLeuGlu
                                                                     AAGATCGGCAAGGCCGGCTACGTGACCGACCGGGCCGGCAGAAGATCGTGAGCCTGACC
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                                                      AAGGAGCCCATCATCGGCGCCCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACC
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                                                                                                                                                                                                                                                                                                                                                                                                               2311 CTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGACGCATCGAT 2358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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млы»; Aspartyl proteäse; Core protein; Hydrolase; Metal-binding;
Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
Zinc-finger.
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Matches:
Conservative:
Mismatches:
InterPro; IPR001037; Integrase_C.
InterPro; IPR001308; Integrase_Zn N.
InterPro; IPR001995; Peptidase_A2.
InterPro; IPR001909; Peptidase_A2.
InterPro; IPR001909; Retrovir matrix.
InterPro; IPR001099; Retrovir matrix.
InterPro; IPR008916; Retrov capsid_N.
InterPro; IPR008919; Retrov capsid_N.
InterPro; IPR008919; Retrov capsid_N.
InterPro; IPR008196; Respective Capsid_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00343; ZNF_C2HC; 2.
PROSITE; PS00141; ASP_PROTRASE; 1.
PROSITE; PS50175; ASP_CHC; 2.
PROSITE; PS50156; ZP_CCHC; 2.
                                                                                                                                                                                                                                            InterPro; IRRO01594; Rve.
InterPro; IRR000147; RvTse.
InterPro; IRR000147; RvTse.
InterPro; IRR000147; RVTse.
InterPro; IRR0010659; RVT_connect.
InterPro; IRR010618; Znf_CCHC.
Pfam; PP00640; Gag_D24; I.
Pfam; PP000075; RasseH; I.
Pfam; PP000075; Rve; I.
Pfam; PP000075; Rve; I.
Pfam; PP000075; RVP; I.
Pfam; PP000075; RVP; I.
Pfam; PP000078; RVP; I.
Pfam; PP06815; RVT_connect; I.
Pfam; PP06815; RVT_connect; I.
Pfam; PP00991; ECCHC; I.
Pfam; PP00991; ECCHC; I.
Pfam; PP00991; ECCHC; I.
Pfam; PP00991; ECCHC; I.
Pfam; PR00939; CZHCZNFINGER.
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96.31%
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                       MEDLINE=22375625; PubMed=12487816; DOI=10.1089/088922202320886325; Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B., Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T., Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L., McCutchan F.E.; Manng 46 near full length HIV type 1 genome sequences from Rakai District, Uganda, subtype D and AD recombinants predominate."; AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                           R HSSP; P447651.

R HSSP; P447651.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:00049012; F:sapartic-type endopeptidase activity; IEA.

R GO; GO:0008907; F:integrase activity; IEA.

R GO; GO:0008233; F:peptidase activity; IEA.

R GO; GO:0008233; F:inbonuclease H activity; IEA.

R GO; GO:0004523; F:ribonuclease H activity; IEA.

R GO; GO:0004523; F:ribonuclease H activity; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0006509; F:sinc ion binding; IEA.

R GO; GO:0006509; P:DNA integration; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR GO; GO:0006509; P:viral life cycle; IEA.
                                                                                                                                                                                                                                                                                                                                                                                          Serwadda S., Sewankambo N., Wabwire F., Kigozi G., Kiwanuka N.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: Belongs to peptidase family A2.
EMBL; AF484491; AAN73556.1; -.
                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kim B., Phillips J.B., Lane J.R., Merling R., McCutchan F.E.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                  Harris M.E., Birx D.L., Robb M.L.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                Lutalo T.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                   Meenen M., Wawer M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001037; Integrase C.
InterPro; IPR0010308; Integrase Zn.
InterPro; IPR001995; Peptidase Az.
InterPro; IPR001909; Peptidase Az.
InterPro; IPR001969; Peptidase Az.
InterPro; IPR001969; Peptidase Az.
InterPro; IPR001099; Retrovir matrix.
InterPro; IPR010999; Retrovir matrix.
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InterPro, IPR008919; Retrov capsid N.
InterPro, IPR002156; RNaseH.
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InterPro; IPR000477; RVTse.
InterPro; IPR010659; RVT_connect.
InterPro; IPR010661; RVT_thumb.
InterPro; IPR011878; Znf_CCHC.
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PF00607; Gag_D24; 1.
PF02022; Integrase_Zn; 1.
PF00075; RnaseH; 1.
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PF00078; RVT 1; 1.
PF06815; RVT_connect; 1.
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Pfam; PF06817; RVT thumb; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00134; Zn-CCHC; 2.
PROSITE; PS00141; ASP PROTEMSE; 1.
PROSITE; PS50158; ZF CCHC; 2.
NON TER 1 1 1
SEQÜENCE 1427 AA; 161058 MW; 20559041E2A88B5C CRC64;
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720
36
25
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                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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3870.50
96.18%
91.60%
84.97%
                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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980 TrpTrpThrAspTyrTrpGlnAlathrTrpIleProGluTrpGluPheValAsnThrPro 1921 CCCCTGGTAAGCTGTACCAGCTGAAAGGAGCCCATCATCGGCGCGAGACCTTC	Qy 2041 CGGGGCGGCAGAAGATCGTGACCTGACCCAACCAGAAGACCGAGAGCTGCAG 2100	Oy 2221 ATCATCGAGCACTGATCAAGAAGGAGAAGGTGTACCTGAGCTGCCCCCCCACAGG 2280	RESULT 15 Q9WF79 ID Q9WF79; AC Q9WF79; DT 01-NOV-1999 (TrEMBLrel. 12, Created) DT 01-NAR-2004 (TrEMBLrel. 12, Last sequence update) DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update) DE Gag-pol polyprotein. OS Human immunodeficiency virus 1.		N. V. V. VIOL. 7, 74427-14939). CC 1- SIMILARITY: Belongs to peptidase family A2. DR EMBL, AF110969; AAD17087.1; DR HSSP, P24736; INCP. DR GO; GO:00019012; C:virion; IEA. DR GO; GO:0001902; C:virion; IEA. DR GO; GO:0003677; F:DNA binding; IEA. DR GO; GO:0003677; F:DNA binding; IEA. DR GO; GO:0003727; F:RNA binding; IEA. DR GO; GO:0003723; F:RNA binding; IEA. DR GO; GO:0003723; F:RNA binding; IEA. DR GO; GO:0003723; F:RNA binding; IEA. DR GO; GO:0003964; F:RNA binding; IEA. DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA. DR GO; GO:0001504; F:Rnasferase activity; IEA. DR GO; GO:0001504; F:Rnasferase activity; IEA. DR GO; GO:0001504; F:Rnasferase activity; IEA. DR GO; GO:0001504; F:Znasferase activity; IEA.
793 ATGGAGAAGGAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACACCCCGTG 852	973 AAGAAGAAGGGTGACCGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCCTG 1032 ::	CAGAGCAGCACAGATCCTGGAGCCTTCCGCGCACCCGCAACCCGGAATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCGTGATCAACCAAGAAGATGATTGAT		ValGlyLysLeuAsnTrpAlaSerGlnIleTyrProGlyIleLysValLysGlnLeuCys AaGCTGCTGCGCGCGCCAAGGCCTGACCGACTTGTGCCCTGACCGAGGGGGGGG	1621 CCCAGCAAGACCTGGTGGCCGAAAGCAGGCCACCACCACGGACCTACCAG 1680 900 ProSerLysAapLeulleAlaGluValGlnLysGlnGlyGlnAspGlnTryTrTyrGln 919 1681 ATCTACCAGGAGCCCTTCAAGAACCTGAAGACGCGCAAGTACGCCAAGATGCGCACCGCC 1740 920 IlleTyrGlnGluProPheLysAsnLeuLysThrGlyLysTyrAlaLysValArgThrAla 939 1741 CACCCAACGACGTGAAGACCTGAAGACGGCAGCAGGAAGATGCCCAAGAGGCACCGCC 1740 940 HisThrAsnAspIleLysGlnLeuThrGluAlaValGlnLysIleAlaArgGluSerIle 959 1801 GTGATCTGGGCACAGACCCCAAGTTCCCCATCCAGAAGACCTGGGAGACC 1860 1801 GTGATCTGGGCACAGACCCCAAGTTCCCCATCCCAGAAGACACCTGGGAGACC 1860 1801 GTGATCTGGGCAAGACCCCCAAGTTCCCCATCCAGAAGACACTCCAGGAGACC 1860 1801 GTGATCTGGGCAAGACCCCCAAGTTCCCCAAGAGACACCTGGGAGACC 1860 1801 GTGATCTGGGCAAGACCCCCAGAGGACACCCCAGAAGACACCCCC 1920

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                          PheProGln11eThrLeuTrpGlnArgProLeuValSerIleLysValGlyGlnIle
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Polyprotein; Protease; RNA-directed DNA polymerase; Transferase; Zinc;
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        replication; IEA.
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Matches:
Conservative:
Mismatches:
Indels:
GO; GO:0006278; P:RNA-dependent DNA rep:
GO; GO:0016032; P:viral life cycle; IEA
R InterPro; IPR001073; Gag_D24.
R InterPro; IPR001037; Integrase_Zn N.
InterPro; IPR001995; Pept.dase_A2.
R InterPro; IPR001995; Pept.dase_A2.
R InterPro; IPR001995; Pept.dase_A2.
R InterPro; IPR001999; Retrovir_matrix.
R InterPro; IPR001999; Retrovir_matrix.
R InterPro; IPR008916; Retrov capsid_N.
R InterPro; IPR008919; Retrov capsid_N.
R InterPro; IPR001999; RNT connect.
R InterPro; IPR001999; Znf_CHC; 2.
R InterPro; IPR00199; Znf_CHC; 2.
R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R InterPro; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR00179; R INTERPRO; IPR0
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96.31%
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84.79%
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Best Local Similarity:
Query Match:
DB:
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SEQUENCE
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	GCGCCCAAGGCCCT rgGlyAlaLyBAlaLe	CCGAGAACCGCGAGAT 	ACCTGGTGGCCGAGAT :::	AGCCCTTCAAGAACCT 	ACGTGAAGCAGCTGAC 	GCAAGACCCCCAAGTT yLysileProLysPh	ACTACTGGCAGGCCAC 	AGCTGTGGTACCAGCT 	GCGCCGCCAACCGCGA 	AGAAGATCGTGAGCCTV ::::: ::: InGluValValThrLe	TGGCCCTGCAGGACAG	GCATCATCCAGGCCCA(AGCTGATCAAGAAGGA 	GCAACGAGCAGATCGA(yAenGluLyeValAs	CCTGGACGGCATCGAT 2358	
	AAGCTGCTGC LysLeuLeuA	CTGGAGCTGG	CCCAGCAAGG	ATCTACCAGG	CACACCAACG	GTGATCTGGG ValileTrpG	TGGTGGACCG	CCCCTGGTGA ProLeuValL	TACGTGGACG	CGGGGCCGGC ::: LysGlyArgG	GCCATCCAGC	TACGCCCTGG	ATCATCGAGC	GGCATCGGCG	TTCCTGGACG	
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US-11-33-413-4

DUBLICATION NO. US20040116660A1

| Publication No. US20040116660A1
| GENERAL INFORMATION:
| APPLICANT: Johnstone, Robert Edward
| APPLICANT: Swanstrom, Rohald Ivar
| APPLICANT: Walliamson, Carolyn
| APPLICANT: Williamson, Carolyn
| TITLE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, Selected H
| TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T:
| TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T:
| TITLE OF INVENTION: NUMBER: US/10/332,413
| CURRENT APPLICATION NUMBER: US/10/332,413
| CURRENT FILING DATE: 2001-07-09
| PRIOR PPLICATION NUMBER: US 60/216,995
| PRIOR APPLICATION NUMBER: ZA 2000/3437
| PRIOR APPLICATION NUMBER: ZA 2000/3437
| PRIOR APPLICATION NUMBER: ZA 2000/4924
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Sequence 3, Appli
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US-10-034-165-9

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US-10-093-953A-31

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US-10-325-468-36

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US-09-725-652-1
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-MODEL=frame+ n2p model - DEV=xlh
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-Q=/CgnZ 1/USF7O spool/US09610313/runat 31052005_155138_15193/app_query.fasta_1.7893
-DB=Published Applications AA -QFWT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -RND=-1 -MATRIX=blosum6Z
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -WODE=LCCAL -OUTFWT=pcto -NORM=ext -HEAPSTZE=500 -MINLEN=0
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-LOOGLCG -DEV TIMEOUT=12 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                    TYPE: PRT ORGANISM: Human immunodeficiency virus type
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 998
                                                                                              Best Local Similarity:
                                                                                       Percent Similarity:
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                                                                 Alignment Scores:
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Percent Similarity:
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US-10-283-847-17
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APPLICANT: Nicolette, Charles A.
APPLICANT: Walker, Bruce
TITLE OF INVENTION: THERAPEUTIC ANTI-HIV (1V9) COMPOUNDS
FILE REFERENCE: 6Z 2112.00
CURRENT APPLICATION NUMBER: US/10/283,847
CURRENT APPLICATION NUMBER: 05/210/293
PRIOR APPLICATION NUMBER: 60/345,116
PRIOR FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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TYPE: PRT
ORGANISM: Human Immunodeficiency
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Sequence 17, Application US/10283847 Publication No. US20030162720A1 GENERAL INFORMATION:

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OTHER INFORMATION: /note= "pol protein of HTLV-III"
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ORGANISM: T cell leukemia-lymphoma virus (HTLV)
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; Publication No. US20050095581A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Nancy T
; APPLICANT: Gallo, Robert C.
; APPLICANT: Wong-Staal, Flossie
; TITLE REFERENCE: 223665
; CURRENT APPLICATION NUMBER: US/10/634,165
; CURRENT APPLICATION NUMBER: US/10/634,165
; CURRENT FILING DATE: 1995-06-05
; PRIOR FILING DATE: 1995-06-05
; PRIOR PILING DATE: 1995-01-23
; PRIOR PILING DATE: 1984-10-10
; PRIOR FILING DATE: 1984-10-10
; PRIOR FILING DATE: 1984-10-10
; PRIOR FILING DATE: 1984-10-10
; RIUNG BAPELICATION NUMBER: 06/659,339
PRIOR PILING DATE: 1984-10-10
; RUMBER OF SEQ ID NOS: 11
; SOFTWARE: PATCHTIN VERSION 3.2
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1306 TTCACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCCTTCCTGCCCATCGAG 1359 	1360 CTGCACCCCAACAAGTGGACCGTGCAGCCCATCGAGCTGCCCGAGAAGGAGAGCTGGACC 1419 	1420 GTGAACGACAAGCTGGTGGGCAAGCTGAACTGGGCCAGCAGATCTACCCCGGC 1479 	O ATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTG 153 [15 48	2	O CACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAG 171	1720 TACGCCAAGATGCGCACCACCACCACCACGAGCAGCTGAAGCAGCTGAGGCCGTGGAG 1779 ::: 521 TyrAlaArgMetArgGlyAlaHisThrAsnAspValLysGlnLeuThrGluAlaValGln 540	18 56	1840 CAGAAGGAGACCTGGGAGACCTGGACTGGACTACTGGCAGGCCACCTGGATCCCCGAG 1899 [9	1960 ATCATCGCCCCGAGACCTTCTACGTGGACGCCCCCCAACCGCGAGACCAAGATCGGC 2019 :::	saccacc 20 ThrThr 64	O AACCAGAAGACCGAGCTGCAGGCCATCCAGGCTGGCCCTGCAGGACAGCGGCAGCGAGGGG 213	21 68	2200 GAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGTACCTG 2259 	2260 AGCTGGGTGCCGCCCACAAGGCATCGGCGGCAACGAGCAGATCGACAAGCTGGTGAGC 2319 :::	2320 AAGGGCATCCGCAAGGTGCTGTTCCTGGACGCATCGAT 2358
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1192 GGCAACCCCGAGATCGTGATCTACCAG-----GCCCCCCTGTACGTGGGCAGCGACCTG 1245
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                   PhelleLysValArgGlnTyrAspGlnIleLeulleGluIleCysGlyHisLysAlaIle
                                                                                  952 ATCCCCCACCCCGCCGGCCTGAAGAAGAAGAGGGGTGACGTGCTGGACGTGGGGGGAC
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TTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATC
                                                                  GGCACCGTGCTGATCGGCCCCCACCCCCGTGAACATCATCGGCCGCAACATGCTGACCCAG
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                                                    GENERAL INFORMATION:
APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Smith, James M.
APPLICANT: Hus, Jian
APPLICANT: Hus, Jian
APPLICANT: Moss, Bernard
APPLICANT: Moss, Bernard
APPLICANT: Wast, Linda
APPLICANT: Watt, Linda
APPLICANTION: AN INMUNE RESPONSE
FILE REFERENCE: 12804-005002
CURRENT APPLICATION NUMBER: US 60/186,364
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR PILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 60/254,845
PRIOR PILING DATE: 2001-03-02
PRIOR PILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR PILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
          Sequence 26, Application US/10093953A Publication No. US20040105871A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                  OTHER INFORMATION: protein encoded by construct of vaccine vector OTHER INFORMATION: pGA1 and vaccine insert expressing clade B HIV-1 OTHER INFORMATION: Gag-Pol
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Matches:
Conservative:
Mismatches:
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/US01/06795
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31
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ORGANISM: Artificial Sequence
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                                         GlnLysGluThrTrpGluThrTrpTrpThrGluTyrTrpGlnAlaThrTrpIleProGlu
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Publication No. US20040105871A1

GENERAL INFORMATION:

APPLICANT: Smith, James M.

APPLICANT: Smith, James M.

APPLICANT: House, James M.

APPLICANT: House, James M.

APPLICANT: Hus, Jian

APPLICANT: Wase, Bernard

APPLICANT: Wase, Bernard

APPLICANT: Wase, Bernard

APPLICANT: Watt, Linda

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING

TITLE OF INVENTION: OMPOSITIONS AND METHODS FOR GENERATING

TITLE OF INVENTION: AND MERR: US/10/093,953A

CURRENT APPLICATION NUMBER: US 60/186,364

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-03-02

PRIOR FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: US 60/251,083

PRIOR FILING DATE: US 000-12-01

PRIOR APPLICATION NUMBER: US 09/798,675
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	CURRENT FILING DATE: 2002-12-19 PRIOR APPLICATION NUMBER: US 60/343,524 PRIOR PILING DATE: 2001-12-21 NUMBER OF SEQ ID NOS: 56 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23 LENGTH: 1003 TYPE: FRT ORGANISW: Artificial Sequence FRATURE: OTHER INFORMATION: recombinant / chimeric sequence: clone 1.10 protein Pol US-10-325-468-23 Alignment Scores: Alignment	Pred. No.: 7.386-157 Length: 1003 1003 1003 1003 1003 1003 1003 1003 1003 1003 1003 1003 1003 1004 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 1006 10
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                                                                                                                                                                                                                                                OTHER INFORMATION: recombinant / chimeric sequence: clone P8A26
## APPLICANT: Soong, Nay Wei

## APPLICANT: Pekrun, Katja

## APPLICANT: Shibata, Ritia

## APPLICANTON MODELS OF HIV-1 PATHOGENESIS

## CURRENT APPLICATION NUMBER: US/10/325,468

## CURRENT PILING DATE: 2002-12-19

## PRIOR PILING DATE: 2001-12-21

## RIOR FILING DATE: 2001-12-21

## RIOR FILING DATE: 2001-12-21

## RIOR FILING DATE: 2001-12-21

## APPLICATION NUMBER

## APPLICANTON NUMBER

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Matches:
Conservative:
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88.07%
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ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
DB:
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Qy 1936 TGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGCGCC 1995 Db 581 TrpTyrGlnLeuGluLysGluProlleValGlyAlaGluThrPheTyrValAspGlyAla 600 Qy 1996 GCCAACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGGACCGCAGAAG 2055 Db 601 AlaAsnargGluThrLysLeuGlyLysAlaGlyTyrValThrSerArgGlyArgGlnLys 620 Qy 2056 ATCGTGAGCTGACCAGCAACCACAAGAACCGAGCTGACGCATCCAGCTGGC 2115 CD 621 ValValSerLeuThrAspGlnLyrAspThrThrAshGlnLysThrGluLeuGlnAlaleHisEleuAla 640	2116 CTGCAGGACAGCGGCAGCGACGTGAACATCGTGACCACAGCCAGTACGCCTGGGCATC	Qy 2176 ATCCAGGCCCAGCCGACAAGAGCGAGAGCGGGTGAACCAGATCATCGAGCAGCTG 2235	Oy 2236 ATCAAGAAGGAGAAGGTTCCTGAGCTGGCGCCCCACAAGGGCATCGGCGCAAC 2295 Db 681 lleLysLysGluLysValTyrLeuThrTtplleProAlaHisLysGlyIleGlyGlyBan 700	Qy 2296 GAGCAGATCGACAAGCTGGTGAGCAAGGGATCCGCAAGGTGCTGCTTCCTGGACGGCATC 2355 Db 701 GluGlnValAspLysLeuValSerAlaGlyIleArgValLeuPheLeuAspGlyIle 720	Qy 2356 GAT 2358 Db 721 Glu 721	RESULT 9 US-10-325-468-9 ; Sequence 9, Application US/10325468	; FUBLICERION NO. USZUG40101823A1 ; GENERAL INFORMATION: ; APPLICANT: Scong, Nay Wei ; APPLICANT: Gerrun, Katja	; TITLE OF INVENTION: HIV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS ; FILE REFERENCE: 0.165_2.10US ; FILE REFERENCE: 0.155_2.10US	; CURRENT AFFLICATION NUMBER: US/10/325,408 ; PRIOR APPLICATION NUMBER: US 60/343,524 ; PRIOR APPLICATION TO 5001112-21	; NUMBER OF SEQ 1D NOS: 30 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 9 ; LENGTH: 1003	ificial Sequence TTON: recombinant / chimeric sequence: clone 1.4 pro	INFORMATION: clone P10.26 protein Pol. 10.00 protein Pol; 468-9	Alignment Scores: 1.03e-156 Length: 1003 Pred. No.: 3384.00 Marches: 634 Percent Similarity: 94.04% Conservative: 44	: 87.93% Mismatches: 74.29% Indels: 16 Gaps:	US-09-610-313B-32 (1-2457) x US-10-325-468-9 (1-1003) Qy 220 TTCTTCCGCGAGGACCTGGCCTTCCCCCAGGGAAAGGCCGCGAGTTCCCCAGCGAGGAG 279	

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US-10-325-468-20
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; Sequence 20, Application US/10325468
; Publication No. US20040101823A1
; GENERAL INFORMATION:
; APPLICANT: Scong, Nay Wei
; APPLICANT: Scong, Nay Wei
; APPLICANT: Schibata, Ritial
; TITLE OF INVENTION: HUV-1 VIRAL VARIANTS FOR IMPROVED ANIMAL
; TITLE OF INVENTION: MODELS OF HIV-1 PATHOGENESIS
; FILE REFERENCE: 0166.210US
; CURRENT APPLICATION NUMBER: US/10/325,468
; FILE APPLICATION NUMBER: US/10/325,468
; PRIOR APPLICATION NUMBER: US 60/343,524
; PRIOR PRILNG DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 20
; SEQ ID NO 20
; LENGTH: 1003
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Matches:
Conservative:
Mismatches:
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94.04%
87.93%
74.29%
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ORGANISM: Artificial Sequence
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Percent Similarity:
Best Local Similarity:
Query Match:
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374 PheLeuTrpMetGlyTyrGluLeuHisProAspArgTrpThrValGlnProlleGluLeu 393 1399 CCCGAGAAGGAGACTGGACCGTGAACGACATCCAGAAGCTGGGGCAAGCTGAACTGG 1458	0 4	1519 434	1579 CGCGAGATCCTGCGGGGCCCCTGCACGGCGTGTACTACGACCCCAGCAAGGACCTGGTG 163	1639 GCCGAGATCCAGAAGCAGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGCCCTTC :::	1699 494	1759	1819	1879	1939 TACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAGACCTTCTACGTGGACGGCGCCGC 1998 	1999 AACCGGGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACC				2239 AAGAAGGAGAAGGTGTACCTGAGCTGGCCGCCCCACAAGGGCATCGGCGCAACGAG 2298 		US-10-296-734-1470 Sequence 1470, Application US/10296734 Fublication No. US20040054137A1 GENERAL INFORMATION. APPLICANT: Thompson, Scott A APPLICANT: Ramshaw, Ian A
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Matches:
Conservative:
Mismatches:
Indels:
   uses
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 14/00
                                                                                             TYPE: PRT ORGANISM: Human immunodeficiency virus
                                                                                                                                        1.21e-155
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93.61%
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: MISC FEATURE
LOCATION: (320)..(320)
OTHER INFORMATION: X = unknown amino acid
  LOCATION: (46)...(46)
OTHER INFORMATION: X = unknown amino acid
                                                                                     LOCATION: (48)...(48)
OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC FEATURE
LOCATION: (51). (51)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (58)...(58)
OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC_FEATURE
LOCATION: (105)..(105)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (130)..(130)
JTHER INFORMATION: X = unknown amino acid
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LOCATION: (300)..(300)
OTHER INFORMATION: X = unknown amino acid
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THER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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THER INFORMATION: X = unknown amino acid
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THER INFORMATION: X = unknown amino acid
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COCATION: (1947)..(194)
OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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THER INFORMATION: X = unknown amino acid
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LOCATION: (293)..(293)
JTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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                                                                                                                              2119 CAGGACAGCGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATC 2178
                                                                 594 SerArgGluThrLysLeuGlyLysAlaGlyTyrValThrAspArgGlyArgGlnLysVal 613
                                                                                                                                                                                                                                            Sequence 1471, Application US/10296734

Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT FILIGATION: UNBER: US/10/296,734

CURRENT FILIAGO ANTE: 2003-08-04

PRIOR PLICATION NUMBER: US/10/296,734

CURRENT FILIAGO ANTE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

LENGTH: 1006
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NAME/KEY: MISC_FEATURE
LOCATION: (15)...(15)
OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: X = unknown amino acid
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NAME/KEY: MISC_PEATURE
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OTHER INFORMATION: X = unknown amino acid
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OTHER INFORMATION: X = unknown amino acid
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LOCATION: (36)...(36)
OTHER INFORMATION: X = unknown amino acid
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LOCATION: (38)...(39)
JTHER INFORMATION: X = unknown amino acid
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THER INFORMATION: X = unknown amino acid
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                                   Length:
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NAME/KEY: MISC FEATURE
LOCATION: (675)...(675)
OTHER INFORMATION: X =
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; TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
; TITLE OF INVENTION: WACCINES EXPRESSING CODON OPTIMIZED HIVI-GAG, POL,
; FILE REPERENCE: 20747Y
; CURRENT APPLICATION NUMBER: US/09/952,060
; CURRENT APPLICATION NUMBER: US/09/14
; PRIOR PELING DATE: 2001-09-14
; PRIOR PILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/273,180
; PRIOR APPLICATION NUMBER: 60/273,180
; PRIOR APPLICATION NUMBER: 60/273,180
; PRIOR PILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PSECSEQ for Windows Version 4.0
; SEQ ID NO 35
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